

03-075-US
SEQUENCE LISTING

<110> Saus, Juan
Revert, Fernando
Revert-Ros, Francisco

<120> Novel Goodpasture antigen-binding protein isoforms and protein misfolded-mediated disorders

<130> 03-075-US

<150> US 60/445,043
<151> 2003-02-05

<150> US 60/445,003
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atg att tgt caa acc ttg gta agc cca cca gag gga aac cag gaa att	2034
Met Ile Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile	
630 635 640 645	
agc agg gac aac att cta tgc aag att aca tat gta gct aat gtg aac	2082
Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn	
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cct gga gga tgg gca cca gcc tca gtg tta agg gca gtg gca aag cga	2130
Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg	
665 670 675	
gag tat cct aaa ttt cta aaa cgt ttt act tct tac gtc caa gaa aaa	2178
Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys	
680 685 690	
act gca gga aag cct att ttg ttc tag tattaaacagg tactagaaga	2225
Thr Ala Gly Lys Pro Ile Leu Phe	
695 700	
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tgttgaaagt atttactatg tttttt	2311

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<211> 701
<212> PRT
<213> Homo sapiens

<400> 8

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Gly Val Thr Ala Thr Ala Ala Ala Asp Gly Trp Lys Gly Arg Leu
20 25 30

Pro Ser Pro Leu Val Leu Leu Pro Arg Ser Ala Arg Cys Gln Ala Arg
35 40 45

Arg Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Leu Pro Pro Thr
50 55 60

Pro Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg
65 70 75 80

Gly Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu
85 90 95

Leu Leu Gly Cys Arg Ala Ser Met Ser Asp Asn Gln Ser Trp Asn Ser
100 105 110

Ser Gly Ser Glu Glu Asp Pro Glu Thr Glu Ser Gly Pro Pro Val Glu
115 120 125

Arg Cys Gly Val Leu Ser Lys Trp Thr Asn Tyr Ile His Gly Trp Gln
130 135 140

Asp Arg Trp Val Val Leu Lys Asn Asn Ala Leu Ser Tyr Tyr Lys Ser
145 150 155 160

Glu Asp Glu Thr Glu Tyr Gly Cys Arg Gly Ser Ile Cys Leu Ser Lys
165 170 175

Ala Val Ile Thr Pro His Asp Phe Asp Glu Cys Arg Phe Asp Ile Ser
180 185 190

Val Asn Asp Ser Val Trp Tyr Leu Arg Ala Gln Asp Pro Asp His Arg
195 200 205

Gln Gln Trp Ile Asp Ala Ile Glu Gln His Lys Thr Glu Ser Gly Tyr
210 215 220

Gly Ser Glu Ser Ser Leu Arg Arg His Gly Ser Met Val Ser Leu Val
225 230 235 240

Ser Gly Ala Ser Gly Tyr Ser Ala Thr Ser Thr Ser Ser Phe Lys Lys
245 250 255

Gly His Ser Leu Arg Glu Lys Leu Ala Glu Met Glu Thr Phe Arg Asp
260 265 270

Ile Leu Cys Arg Gln Val Asp Thr Leu Gln Lys Tyr Phe Asp Ala Cys
 275 280 285

Ala Asp Ala Val Ser Lys Asp Glu Leu Gln Arg Asp Lys Val Val Glu
 290 295 300

Asp Asp Glu Asp Asp Phe Pro Thr Thr Arg Ser Asp Gly Asp Phe Leu
 305 310 315 320

His Ser Thr Asn Gly Asn Lys Glu Lys Leu Phe Pro His Val Thr Pro
 325 330 335

Lys Gly Ile Asn Gly Ile Asp Phe Lys Gly Glu Ala Ile Thr Phe Lys
 340 345 350

Ala Thr Thr Ala Gly Ile Leu Ala Thr Leu Ser His Cys Ile Glu Leu
 355 360 365

Met Val Lys Arg Glu Asp Ser Trp Gln Lys Arg Leu Asp Lys Glu Thr
 370 375 380

Glu Lys Lys Arg Arg Thr Glu Glu Ala Tyr Lys Asn Ala Met Thr Glu
 385 390 395 400

Leu Lys Lys Ser His Phe Gly Gly Pro Asp Tyr Glu Glu Gly Pro
 405 410 415

Asn Ser Leu Ile Asn Glu Glu Glu Phe Phe Asp Ala Val Glu Ala Ala
 420 425 430

Leu Asp Arg Gln Asp Lys Ile Glu Glu Gln Ser Gln Ser Glu Lys Val
 435 440 445

Arg Leu His Trp Pro Thr Ser Leu Pro Ser Gly Asp Ala Phe Ser Ser
 450 455 460

Val Gly Thr His Arg Phe Val Gln Lys Val Glu Glu Met Val Gln Asn
 465 470 475 480

His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala Asn Trp Gln
 485 490 495

Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg Glu Val Glu
 500 505 510

Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His Ala Val Lys
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515

520

525

Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn Val Asp Val
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Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val Val Glu Thr
545 550 555 560

Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys Arg Val Trp
565 570 575

Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile Arg Lys Ile
580 585 590

Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val Cys Asn Phe
595 600 605

Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys Val Arg Ala
610 615 620

Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro Pro Glu
625 630 635 640

Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr Tyr
645 650 655

Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg
660 665 670

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48

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tct ggg ccg cct gtg gag cgc tgc ggg gtc ctc agt aag tgg aca aac				144
Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr Asn				
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tac att cat ggg tgg cag gat cgt tgg gta gtt ttg aaa aat aat gct				192
Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn Ala				
50 55 60				
ctg agt tac tac aaa tct gaa gat gaa aca gag tat ggc tgc aga gga				240
Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys Arg Gly				
65 70 75 80				
tcc atc tgt ctt agc aag gct gtc atc aca cct cac gat ttt gat gaa				288
Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp Glu				
85 90 95				
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Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg Ala				
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Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu Gln His				
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Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg His Gly				
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Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala Thr Ser				
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Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu Leu Gln				
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Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr Thr Arg				
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Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe Lys Gly				
245 250 255				
gaa gcg ata act ttt aaa gca act act gct gga atc ctt gca aca ctt				816

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Glu	Ala	Ile	Thr	Phe	Lys	Ala	Thr	Thr	Ala	Gly	Ile	Leu	Ala	Thr	Leu
260						265			270						
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Ser	His	Cys	Ile	Glu	Leu	Met	Val	Lys	Arg	Glu	Asp	Ser	Trp	Gln	Lys
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Arg	Leu	Asp	Lys	Glu	Thr	Glu	Lys	Lys	Arg	Arg	Thr	Glu	Glu	Ala	Tyr
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Lys	Asn	Ala	Met	Thr	Glu	Leu	Lys	Lys	Lys	Ser	His	Phe	Gly	Gly	Pro
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gat	tat	gaa	gaa	ggc	cct	aac	agt	ctg	att	aat	gaa	gaa	gag	ttc	ttt
Asp	Tyr	Glu	Glu	Gly	Pro	Asn	Ser	Leu	Ile	Asn	Glu	Glu	Phe	Phe	
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gat	gct	gtt	gaa	gct	gct	ctt	gac	aga	caa	gat	aaa	ata	gaa	gaa	cag
Asp	Ala	Val	Glu	Ala	Ala	Leu	Asp	Arg	Gln	Asp	Lys	Ile	Glu	Glu	Gln
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tca	cag	agt	gaa	aag	gtg	aga	tta	cat	tgg	cct	aca	tcc	ttg	ccc	tct
Ser	Gln	Ser	Glu	Lys	Val	Arg	Leu	His	Trp	Pro	Thr	Ser	Leu	Pro	Ser
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gga	gat	gcc	ttt	tct	tct	gtg	ggg	aca	cat	aga	ttt	gtc	caa	aag	ccc
Gly	Asp	Ala	Phe	Ser	Ser	Val	Gly	Thr	His	Arg	Phe	Val	Gln	Lys	Pro
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Tyr	Ser	Arg	Ser	Ser	Ser	Met	Ser	Ser	Ile	Asp	Leu	Val	Ser	Ala	Ser
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Asp	Asp	Val	His	Arg	Phe	Ser	Ser	Gln	Val	Glu	Glu	Met	Val	Gln	Asn
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cac	atg	act	tac	tca	tta	cag	gat	gta	ggc	gga	gat	gcc	aat	tgg	cag
His	Met	Thr	Tyr	Ser	Leu	Gln	Asp	Val	Gly	Gly	Asp	Ala	Asn	Trp	Gln
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Leu	Val	Val	Glu	Glu	Gly	Glu	Met	Lys	Val	Tyr	Arg	Arg	Glu	Val	Glu
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Glu	Asn	Gly	Ile	Val	Leu	Asp	Pro	Leu	Lys	Ala	Thr	His	Ala	Val	Lys
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Gly	Val	Thr	Gly	His	Glu	Val	Cys	Asn	Tyr	Phe	Trp	Asn	Val	Asp	Val
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cgc	aat	gac	tgg	gaa	aca	act	ata	gaa	aac	ttt	cat	gtg	gtg	gaa	aca
Arg	Asn	Asp	Trp	Glu	Thr	Thr	Ile	Glu	Asn	Phe	His	Val	Val	Glu	Thr
485						490			495						
tta	gct	gat	aat	gca	atc	atc	att	tat	caa	aca	cac	aag	agg	gtg	tgg
Leu	Ala	Asp	Asn	Ala	Ile	Ile	Ile	Tyr	Gln	Thr	His	Lys	Arg	Val	Trp
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cca gcc ttg act gaa aat gac cct gaa act tgg ata gtt tgt aat ttt Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val Cys Asn Phe 530 535 540	1632
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Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn Ala
50 55 60

Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys Arg Gly
65 70 75 80

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Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp Glu
85 90 95

Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg Ala
100 105 110

Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu Gln His
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Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg His Gly
130 135 140

Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala Thr Ser
145 150 155 160

Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu Ala Glu
165 170 175

Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr Leu Gln
180 185 190

Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu Leu Gln
195 200 205

Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr Thr Arg
210 215 220

Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu Lys Leu
225 230 235 240

Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe Lys Gly
245 250 255

Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala Thr Leu
260 265 270

Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp Gln Lys
275 280 285

Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu Ala Tyr
290 295 300

Lys Asn Ala Met Thr Glu Leu Lys Lys Ser His Phe Gly Gly Pro
305 310 315 320

Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu Phe Phe
325 330 335

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Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu Glu Gln
340 345 350

Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu Pro Ser
355 360 365

Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln Lys Pro
370 375 380

Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val Ser Ala Ser
385 390 395 400

Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met Val Gln Asn
405 410 415

His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala Asn Trp Gln
420 425 430

Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg Glu Val Glu
435 440 445

Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His Ala Val Lys
450 455 460

Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn Val Asp Val
465 470 475 480

Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val Val Glu Thr
485 490 495

Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys Arg Val Trp
500 505 510

Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile Arg Lys Ile
515 520 525

Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val Cys Asn Phe
530 535 540

Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys Val Arg Ala
545 550 555 560

Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro Pro Glu
565 570 575

Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr Tyr
580 585 590

Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg
595 600 605

Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr Ser
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20 25 30		
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Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr Asn		
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Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn Ala		
50 55 60		
ctg agt tac tac aaa tct gaa gat gaa aca gag tat ggc tgc aga gga		240
Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys Arg Gly		
65 70 75 80		
tcc atc tgt ctt agc aag gct gtc atc aca cct cac gat ttt gat gaa		288
Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp Glu		
85 90 95		
tgt cga ttt gat att agt gta aat gat agt gtt tgg tat ctt cgt gct		336
Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg Ala		
100 105 110		
cag gat cca gat cat aga cag caa tgg ata gat gcc att gaa cag cac		384
Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu Gln His		
115 120 125		
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Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg His Gly		
130 135 140		

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acc tct tca ttc aag aaa ggc cac agt tta cgt gag aag ttg gct gaa	528
Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu Ala Glu	
165 170 175	
atg gaa aca ttt aga gac atc tta tgt aga caa gtt gac acg cta cag	576
Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr Leu Gln	
180 185 190	
aag tac ttt gat gcc tgt gct gat gct gtc tct aag gat gaa ctt caa	624
Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu Leu Gln	
195 200 205	
agg gat aaa gtg gta gaa gat gat gaa gat gac ttt cct aca acg cgt	672
Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr Thr Arg	
210 215 220	
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Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu Lys Leu	
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Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe Lys Gly	
245 250 255	
gaa gcg ata act ttt aaa gca act act gct gga atc ctt gca aca ctt	816
Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala Thr Leu	
260 265 270	
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Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp Gln Lys	
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Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu Ala Tyr	
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Lys Asn Ala Met Thr Glu Leu Lys Lys Ser His Phe Gly Gly Pro	
305 310 315 320	
gat tat gaa gaa ggc cct aac agt ctg att aat gaa gaa gag ttc ttt	1008
Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu Phe Phe	
325 330 335	
gat gct gtt gaa gct gct ctt gac aga caa gat aaa ata gaa gaa cag	1056
Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu Glu Gln	
340 345 350	
tca cag agt gaa aag gtg aga tta cat tgg cct aca tcc ttg ccc tct	1104
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355 360 365	
gga gat gcc ttt tct tct gtg ggg aca cat aga ttt gtc caa aag gtt	1152
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Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly	

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ttg gta agc cca cca gag gga aac cag gaa att agc agg gac aac att Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile 545 550 555 560			1680
cta tgc aag att aca tat gta gct aat gtg aac cct gga gga tgg gca Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala 565 570 575			1728
cca gcc tca gtg tta agg gca gtg gca aag cga gag tat cct aaa ttt Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe 580 585 590			1776
cta aaa cgt ttt act tct tac gtc caa gaa aaa act gca gga aag cct Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro 595 600 605			1824
att ttg ttc tag Ile Leu Phe 610			1836

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 <212> PRT
 <213> artificial

<220>

<223> Derived sequence

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20 25 30

Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr Asn
35 40 45

Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn Ala
50 55 60

Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys Arg Gly
65 70 75 80

Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp Glu
85 90 95

Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg Ala
100 105 110

Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu Gln His
115 120 125

Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg His Gly
130 135 140

Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala Thr Ser
145 150 155 160

Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu Ala Glu
165 170 175

Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr Leu Gln
180 185 190

Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu Leu Gln
195 200 205

Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr Thr Arg
210 215 220

Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu Lys Leu
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225	230	235	240
Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe Lys Gly			
245	250	255	
Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala Thr Leu			
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Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp Gln Lys			
275	280	285	
Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu Ala Tyr			
290	295	300	
Lys Asn Ala Met Thr Glu Leu Lys Lys Ser His Phe Gly Gly Pro			
305	310	315	320
Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu Phe Phe			
325	330	335	
Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu Glu Gln			
340	345	350	
Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu Pro Ser			
355	360	365	
Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln Lys Val			
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Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly			
385	390	395	400
Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val			
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Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys			
420	425	430	
Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr			
435	440	445	
Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn			
450	455	460	
Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln			
465	470	475	480

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Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu
 485 490 495

Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr
 500 505 510

Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn
 515 520 525

Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr
 530 535 540

Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile
 545 550 555 560

Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala
 565 570 575

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 595 600 605

Ile Leu Phe
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tcg gat aat cag agc tgg aac tcg tcg ggc tcg gag gag gat cca gag Ser Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro Glu 35 40 45	144
acg gag tct ggg ccg cct gtg gag cgc tgc ggg gtc ctc agt aag tgg	192

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Thr	Glu	Ser	Gly	Pro	Pro	Val	Glu	Arg	Cys	Gly	Val	Leu	Ser	Lys	Trp	
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Thr	Asn	Tyr	Ile	His	Gly	Trp	Gln	Asp	Arg	Trp	Val	Val	Leu	Lys	Asn	
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aat	gct	ctg	agt	tac	tac	aaa	tct	gaa	gat	gaa	aca	gag	tat	ggc	tgc	288
Asn	Ala	Leu	Ser	Tyr	Tyr	Lys	Ser	Glu	Asp	Glu	Thr	Glu	Tyr	Gly	Cys	
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aga	gga	tcc	atc	tgt	ctt	agc	aag	gct	gtc	atc	aca	cct	cac	gat	ttt	336
Arg	Gly	Ser	Ile	Cys	Leu	Ser	Lys	Ala	Val	Ile	Thr	Pro	His	Asp	Phe	
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gat	gaa	tgt	cga	ttt	gat	att	agt	gta	aat	gat	agt	gtt	tgg	tat	ctt	384
Asp	Glu	Cys	Arg	Phe	Asp	Ile	Ser	Val	Asn	Asp	Ser	Val	Trp	Tyr	Leu	
						115			120			125				
cgt	gct	cag	gat	cca	gat	cat	aga	cag	caa	tgg	ata	gat	gcc	att	gaa	432
Arg	Ala	Gln	Asp	Pro	Asp	His	Arg	Gln	Gln	Trp	Ile	Asp	Ala	Ile	Glu	
						130			135			140				
cag	cac	aag	act	gaa	tct	gga	tat	gga	tct	gaa	tcc	agc	ttg	cgt	cga	480
Gln	His	Lys	Thr	Glu	Ser	Gly	Tyr	Gly	Ser	Glu	Ser	Ser	Leu	Arg	Arg	
						145			150			155			160	
cat	ggc	tca	atg	gtg	tcc	ctg	gtg	tct	gga	gca	agt	ggc	tac	tct	gca	528
His	Gly	Ser	Met	Val	Ser	Leu	Val	Ser	Gly	Ala	Ser	Gly	Tyr	Ser	Ala	
						165			170			175				
aca	tcc	acc	tct	tca	ttc	aag	aaa	ggc	cac	agt	tta	cgt	gag	aag	ttg	576
Thr	Ser	Thr	Ser	Ser	Phe	Lys	Lys	Gly	His	Ser	Leu	Arg	Glu	Lys	Leu	
						180			185			190				
gct	gaa	atg	gaa	aca	ttt	aga	gac	atc	tta	tgt	aga	caa	gtt	gac	acg	624
Ala	Glu	Met	Glu	Thr	Phe	Arg	Asp	Ile	Leu	Cys	Arg	Gln	Val	Asp	Thr	
						195			200			205				
cta	cag	aag	tac	ttt	gat	gcc	tgt	gct	gat	gct	tct	aag	gat	gaa	672	
Leu	Gln	Lys	Tyr	Phe	Asp	Ala	Cys	Ala	Asp	Ala	Val	Ser	Lys	Asp	Glu	
						210			215			220				
ctt	caa	agg	gat	aaa	gtg	gta	gaa	gat	gat	gaa	gat	gac	ttt	cct	aca	720
Leu	Gln	Arg	Asp	Lys	Val	Val	Glu	Asp	Asp	Glu	Asp	Asp	Phe	Pro	Thr	
						225			230			235			240	
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Lys	Gly	Glu	Ala	Ile	Thr	Phe	Lys	Ala	Thr	Thr	Ala	Gly	Ile	Leu	Ala	
						275			280			285				
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Thr	Leu	Ser	His	Cys	Ile	Glu	Leu	Met	Val	Lys	Arg	Glu	Asp	Ser	Trp	
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Gln	Lys	Arg	Leu	Asp	Lys	Glu	Thr	Glu	Lys	Lys	Arg	Arg	Thr	Glu	Glu	
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gca	tat	aaa	aat	gca	atg	aca	gaa	ctt	aag	aaa	aaa	tcc	cac	ttt	gga	1008
Ala	Tyr	Lys	Asn	Ala	Met	Thr	Glu	Leu	Lys	Lys	Lys	Ser	His	Phe	Gly	
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Gly	Pro	Asp	Tyr	Glu	Glu	Gly	Pro	Asn	Ser	Leu	Ile	Asn	Glu	Glu	Glu	
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Phe	Phe	Asp	Ala	Val	Glu	Ala	Ala	Leu	Asp	Arg	Gln	Asp	Lys	Ile	Glu	
					355			360							365	
gaa	cag	tca	cag	agt	gaa	aag	gtg	aga	tta	cat	tgg	cct	aca	tcc	ttg	1152
Glu	Gln	Ser	Gln	Ser	Glu	Lys	Val	Arg	Leu	His	Trp	Pro	Thr	Ser	Leu	
					370			375			380					
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Pro	Ser	Gly	Asp	Ala	Phe	Ser	Ser	Val	Gly	Thr	His	Arg	Phe	Val	Gln	
					385			390			395				400	
aag	ccc	tat	agt	cgc	tct	tcc	atg	tct	tcc	att	gat	cta	gtc	agt		1248
Lys	Pro	Tyr	Ser	Arg	Ser	Ser	Ser	Met	Ser	Ser	Ile	Asp	Leu	Val	Ser	
					405				410						415	
gcc	tct	gat	gat	gtt	cac	aga	ttc	agc	tcc	cag	gtt	gaa	gag	atg	gtg	1296
Ala	Ser	Asp	Asp	Val	His	Arg	Phe	Ser	Ser	Gln	Val	Glu	Glu	Met	Val	
					420			425							430	
cag	aac	cac	atg	act	tac	tca	tta	cag	gat	gta	ggc	gga	gat	gcc	aat	1344
Gln	Asn	His	Met	Thr	Tyr	Ser	Leu	Gln	Asp	Val	Gly	Gly	Asp	Ala	Asn	
					435			440							445	
tgg	cag	ttg	gtt	gta	gaa	gaa	gga	gaa	atg	aag	gta	tac	aga	aga	gaa	1392
Trp	Gln	Leu	Val	Val	Glu	Glu	Gly	Glu	Met	Lys	Val	Tyr	Arg	Arg	Glu	
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Val	Glu	Glu	Asn	Gly	Ile	Val	Leu	Asp	Pro	Leu	Lys	Ala	Thr	His	Ala	
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Asp	Val	Arg	Asn	Asp	Trp	Glu	Thr	Thr	Ile	Glu	Asn	Phe	His	Val	Val	
					500			505							510	
gaa	aca	tta	gct	gat	aat	gca	atc	atc	att	tat	caa	aca	cac	aag	agg	1584
Glu	Thr	Leu	Ala	Asp	Asn	Ala	Ile	Ile	Ile	Tyr	Gln	Thr	His	Lys	Arg	
					515			520							525	
gtg	tgg	cct	gct	tct	cag	cga	gac	gta	tta	tat	ctt	tct	gtc	att	cga	1632
Val	Trp	Pro	Ala	Ser	Gln	Arg	Asp	Val	Leu	Tyr	Leu	Ser	Val	Ile	Arg	
					530			535			540					
aag	ata	cca	gcc	ttg	act	gaa	aat	gac	cct	gaa	act	tgg	ata	gtt	tgt	1680
Lys	Ile	Pro	Ala	Leu	Thr	Glu	Asn	Asp	Pro	Glu	Thr	Trp	Ile	Val	Cys	
					545			550			555				560	

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Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys Val	
565 570 575	
cgt gcc aaa ata aat gtt gct atg att tgt caa acc ttg gta agc cca	1776
Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro	
580 585 590	
cca gag gga aac cag gaa att agc agg gac aac att cta tgc aag att	1824
Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile	
595 600 605	
aca tat gta gct aat gtg aac cct gga gga tgg gca cca gcc tca gtg	1872
Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val	
610 615 620	
tta agg gca gtg gca aag cga gag tat cct aaa ttt cta aaa cgt ttt	1920
Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe	
625 630 635 640	
act tct tac gtc caa gaa aaa act gca gga aag cct att ttg ttc tag	1968
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<223> Derived sequence

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20 25 30

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35 40 45

Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp
50 55 60

Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn
65 70 75 80

Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys
85 90 95

Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe
100 105 110

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Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu
115 120 125

Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu
130 135 140

Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg
145 150 155 160

His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala
165 170 175

Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu
180 185 190

Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr
195 200 205

Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu
210 215 220

Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr
225 230 235 240

Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu
245 250 255

Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe
260 265 270

Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala
275 280 285

Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp
290 295 300

Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu
305 310 315 320

Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe Gly
325 330 335

Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu
340 345 350

Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu
355 360 365

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Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu
370 375 380

Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln
385 390 395 400

Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val Ser
405 410 415

Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met Val
420 425 430

Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala Asn
435 440 445

Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg Glu
450 455 460

Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His Ala
465 470 475 480

Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn Val
485 490 495

Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val Val
500 505 510

Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys Arg
515 520 525

Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile Arg
530 535 540

Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val Cys
545 550 555 560

Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys Val
565 570 575

Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro
580 585 590

Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile
595 600 605

Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val
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610

615

620

Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe
 625 630 635 640

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 645 650 655

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 Ala Glu Gly Ala Gly Ala Gly Leu Leu Leu Gly Cys Arg Ala Ser Met
 20 25 30

tcg gat aat cag agc tgg aac tcg tcg ggc tcg gag gag gat cca gag 144
 Ser Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro Glu
 35 40 45

acg gag tct ggg ccg cct gtg gag cgc tgc ggg gtc ctc agt aag tgg 192
 Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp
 50 55 60

aca aac tac att cat ggg tgg cag gat cgt tgg gta gtt ttg aaa aat 240
 Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn
 65 70 75 80

aat gct ctg agt tac tac aaa tct gaa gat gaa aca gag tat ggc tgc 288
 Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys
 85 90 95

aga gga tcc atc tgt ctt agc aag gct gtc atc aca cct cac gat ttt 336
 Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe
 100 105 110

gat gaa tgt cga ttt gat att agt gta aat gat agt gtt tgg tat ctt 384
 Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu
 115 120 125

cgt gct cag gat cca gat cat aga cag caa tgg ata gat gcc att gaa 432
 Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu
 130 135 140

cag cac aag act gaa tct gga tat gga tct gaa tcc agc ttg cgt cga 480
 Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg

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145	150	155	160	
cat ggc tca atg gtg tcc ctg gtg tct gga gca agt ggc tac tct gca				528
His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala				
165	170	175		
aca tcc acc tct tca ttc aag aaa ggc cac agt tta cgt gag aag ttg				576
Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu				
180	185	190		
gct gaa atg gaa aca ttt aga gac atc tta tgt aga caa gtt gac acg				624
Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr				
195	200	205		
cta cag aag tac ttt gat gcc tgt gct gat gct gtc tct aag gat gaa				672
Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu				
210	215	220		
ctt caa agg gat aaa gtg gta gaa gat gat gaa gat gac ttt cct aca				720
Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr				
225	230	235	240	
acg cgt tct gat ggt gac ttc ttg cat agt acc aac ggc aat aaa gaa				768
Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu				
245	250	255		
aag tta ttt cca cat gtg aca cca aaa gga att aat ggt ata gac ttt				816
Lys Leu Phe Pro His Val Thr Pro Lys Gln Ile Asn Gly Ile Asp Phe				
260	265	270		
aaa ggg gaa gcg ata act ttt aaa gca act act gct gga atc ctt gca				864
Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala				
275	280	285		
aca ctt tct cat tgt att gaa cta atg gtt aaa cgt gag gac agc tgg				912
Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp				
290	295	300		
cag aag aga ctg gat aag gaa act gag aag aaa aga aga aca gag gaa				960
Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu				
305	310	315	320	
gca tat aaa aat gca atg aca gaa ctt aag aaa aaa tcc cac ttt gga				1008
Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Ser His Phe Gly				
325	330	335		
gga cca gat tat gaa gaa ggc cct aac agt ctg att aat gaa gaa gag				1056
Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu				
340	345	350		
ttc ttt gat gct gtt gaa gct gct ctt gac aga caa gat aaa ata gaa				1104
Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu				
355	360	365		
gaa cag tca cag agt gaa aag gtg aga tta cat tgg cct aca tcc ttg				1152
Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu				
370	375	380		
ccc tct gga gat gcc ttt tct tct gtg ggg aca cat aga ttt gtc caa				1200
Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln				
385	390	395	400	
aag gtt gaa gag atg gtg cag aac cac atg act tac tca tta cag gat				1248

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Lys Val Glu Glu Met Val Gln Asn His	Met Thr Tyr Ser Leu Gln Asp		
405	410	415	
gta ggc gga gat gcc aat tgg cag ttg gtt gta gaa gaa gga gaa atg		1296	
Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met			
420	425	430	
aag gta tac aga aga gaa gta gaa gaa aat ggg att gtt ctg gat cct		1344	
Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro			
435	440	445	
tta aaa gct acc cat gca gtt aaa ggc gtc aca gga cat gaa gtc tgc		1392	
Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val Cys			
450	455	460	
aat tat ttc tgg aat gtt gac gtt cgc aat gac tgg gaa aca act ata		1440	
Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile			
465	470	475	480
gaa aac ttt cat gtg gtg gaa aca tta gct gat aat gca atc atc att		1488	
Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile			
485	490	495	
tat caa aca cac aag agg gtg tgg cct gct tct cag cga gac gta tta		1536	
Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu			
500	505	510	
tat ctt tct gtc att cga aag ata cca gcc ttg act gaa aat gac cct		1584	
Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro			
515	520	525	
gaa act tgg ata gtt tgt aat ttt tct gtg gat cat gac agt gct cct		1632	
Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro			
530	535	540	
cta aac aac cga tgt gtc cgt gcc aaa ata aat gtt gct atg att tgt		1680	
Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys			
545	550	555	560
caa acc ttg gta agc cca cca gag gga aac cag gaa att agc agg gac		1728	
Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp			
565	570	575	
aac att cta tgc aag att aca tat gta gct aat gtg aac cct gga gga		1776	
Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly			
580	585	590	
tgg gca cca gcc tca gtg tta agg gca gtg gca aag cga gag tat cct		1824	
Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro			
595	600	605	
aaa ttt cta aaa cgt ttt act tct tac gtc caa gaa aaa act gca gga		1872	
Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly			
610	615	620	
aag cct att ttg ttc tag		1890	
Lys Pro Ile Leu Phe			
625			

<210> 16
<211> 629
<212> PRT

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<213> artificial

<220>

<223> Derived sequence

<400> 16

Pro Ser Pro Asp Pro Ser Pro Arg Gly Leu Gly Ala Ser Ser Gly Ala
1 5 10 15

Ala Glu Gly Ala Gly Ala Gly Leu Leu Leu Gly Cys Arg Ala Ser Met
20 25 30

Ser Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro Glu
35 40 45

Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp
50 55 60

Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn
65 70 75 80

Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys
85 90 95

Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe
100 105 110

Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu
115 120 125

Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu
130 135 140

Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg
145 150 155 160

His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala
165 170 175

Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu
180 185 190

Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr
195 200 205

Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu
210 215 220

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Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr
225 230 235 240

Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu
245 250 255

Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe
260 265 270

Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala
275 280 285

Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp
290 295 300

Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu
305 310 315 320

Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe Gly
325 330 335

Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu
340 345 350

Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu
355 360 365

Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu
370 375 380

Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln
385 390 395 400

Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp
405 410 415

Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met
420 425 430

Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro
435 440 445

Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val Cys
450 455 460

Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile
465 470 475 480

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Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile
485 490 495

Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu
500 505 510

Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro
515 520 525

Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro
530 535 540

Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys
545 550 555 560

Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp
565 570 575

Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly
580 585 590

Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro
595 600 605

Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly
610 615 620

Lys Pro Ile Leu Phe
625

<210> 17

<211> 2037

<212> DNA

<213> artificial

<220>

<223> Derived sequence

<220>

<221> CDS

<222> (1)..(2037)

<223>

<400> 17

cgg cgc ggc ggg cg^g act tcg tcc ctc ctc ctg ctc ccc ccc aca ccg 48
Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Pro Pro Thr Pro
1 5 10 15

gag cgg gca ctc ttc gct tcg cca tcc ccc gac cct tca ccc cga gga 96
Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
20 25 30

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ctg	ggc	gcc	tcc	tcc	ggc	gca	gct	gag	gga	gcy	ggg	gcc	ggt	ctc	ctg	144
Leu	Gly	Ala	Ser	Ser	Gly	Ala	Ala	Glu	Gly	Ala	Gly	Ala	Gly	Leu	Leu	
35					40					45						
ctc	ggt	tgt	cga	gcc	tcc	atg	tcg	gat	aat	cag	agc	tgg	aac	tcg	tcg	192
Leu	Gly	Cys	Arg	Ala	Ser	Met	Ser	Asp	Asn	Gln	Ser	Trp	Asn	Ser	Ser	
50					55					60						
ggc	tcg	gag	gag	gat	cca	gag	acg	gag	tct	ggg	ccg	cct	gtg	gag	cgc	240
Gly	Ser	Glu	Glu	Asp	Pro	Glu	Thr	Glu	Ser	Gly	Pro	Pro	Val	Glu	Arg	
65					70				75					80		
tgc	ggg	gtc	ctc	agt	aag	tgg	aca	aac	tac	att	cat	ggg	tgg	cag	gat	288
Cys	Gly	Val	Leu	Ser	Lys	Trp	Thr	Asn	Tyr	Ile	His	Gly	Trp	Gln	Asp	
85					90				95							
cgt	tgg	gta	gtt	ttg	aaa	aat	aat	gct	ctg	agt	tac	tac	aaa	tct	gaa	336
Arg	Trp	Val	Val	Leu	Lys	Asn	Asn	Ala	Leu	Ser	Tyr	Tyr	Lys	Ser	Glu	
100					105								110			
gat	gaa	aca	gag	tat	ggc	tgc	aga	gga	tcc	atc	tgt	ctt	agc	aag	gct	384
Asp	Glu	Thr	Glu	Tyr	Gly	Cys	Arg	Gly	Ser	Ile	Cys	Leu	Ser	Lys	Ala	
115					120					125						
gtc	atc	aca	cct	cac	gat	ttt	gat	gaa	tgt	cga	ttt	gat	att	agt	gta	432
Val	Ile	Thr	Pro	His	Asp	Phe	Asp	Glu	Cys	Arg	Phe	Asp	Ile	Ser	Val	
130					135					140						
aat	gat	agt	gtt	tgg	tat	ctt	cgt	gct	cag	gat	cca	gat	cat	aga	cag	480
Asn	Asp	Ser	Val	Trp	Tyr	Leu	Arg	Ala	Gln	Asp	Pro	Asp	His	Arg	Gln	
145					150				155				160			
caa	tgg	ata	gat	gcc	att	gaa	cag	cac	aag	act	gaa	tct	gga	tat	gga	528
Gln	Trp	Ile	Asp	Ala	Ile	Glu	Gln	His	Lys	Thr	Glu	Ser	Gly	Tyr	Gly	
165					170				175							
tct	gaa	tcc	agc	ttg	cgt	cga	cat	ggc	tca	atg	gtg	tcc	ctg	gtg	tct	576
Ser	Glu	Ser	Leu	Arg	Arg	His	Gly	Ser	Met	Val	Ser	Leu	Val	Ser		
180					185					190						
gga	gca	agt	ggc	tac	tct	gca	aca	tcc	acc	tct	tca	ttc	aag	aaa	ggc	624
Gly	Ala	Ser	Gly	Tyr	Ser	Ala	Thr	Ser	Thr	Ser	Ser	Phe	Lys	Lys	Gly	
195					200					205						
cac	agt	tta	cgt	gag	aag	ttg	gct	gaa	atg	gaa	aca	ttt	aga	gac	atc	672
His	Ser	Leu	Arg	Glu	Lys	Leu	Ala	Glu	Met	Glu	Thr	Phe	Arg	Asp	Ile	
210					215					220						
tta	tgt	aga	caa	gtt	gac	acg	cta	cag	aag	tac	ttt	gat	gcc	tgt	gct	720
Leu	Cys	Arg	Gln	Val	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	Asp	Ala	Cys	Ala	
225					230				235				240			
gat	gct	gtc	tct	aag	gat	gaa	ctt	caa	agg	gat	aaa	gtg	gta	gaa	gat	768
Asp	Ala	Val	Ser	Lys	Asp	Glu	Leu	Gln	Arg	Asp	Lys	Val	Val	Glu	Asp	
245					250					255						
gat	gaa	gat	gac	ttt	cct	aca	acg	cgt	tct	gat	ggt	gac	ttc	ttg	cat	816
Asp	Glu	Asp	Asp	Phe	Pro	Thr	Thr	Arg	Ser	Asp	Gly	Asp	Phe	Leu	His	
260					265					270						
agt	acc	aac	ggc	aat	aaa	gaa	aag	tta	ttt	cca	cat	gtg	aca	cca	aaa	864
Ser	Thr	Asn	Gly	Asn	Lys	Glu	Lys	Leu	Phe	Pro	His	Val	Thr	Pro	Lys	
275					280					285						

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gga att aat ggt ata gac ttt aaa ggg gaa gcg ata act ttt aaa gca Gly Ile Asn Gly Ile Asp Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala 290 295 300	912
act act gct gga atc ctt gca aca ctt tct cat tgt att gaa cta atg Thr Thr Ala Gly Ile Leu Ala Thr Leu Ser His Cys Ile Glu Leu Met 305 310 315 320	960
gtt aaa cgt gag gac agc tgg cag aag aga ctg gat aag gaa act gag Val Lys Arg Glu Asp Ser Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu 325 330 335	1008
aag aaa aga aga aca gag gaa gca tat aaa aat gca atg aca gaa ctt Lys Lys Arg Arg Thr Glu Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu 340 345 350	1056
aag aaa aaa tcc cac ttt gga gga cca gat tat gaa gaa ggc cct aac Lys Lys Lys Ser His Phe Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn 355 360 365	1104
agt ctg att aat gaa gaa gag ttc ttt gat gct gtt gaa gct gct ctt Ser Leu Ile Asn Glu Glu Phe Phe Asp Ala Val Glu Ala Ala Leu 370 375 380	1152
gac aga caa gat aaa ata gaa gaa cag tca cag agt gaa aag gtg aga Asp Arg Gln Asp Lys Ile Glu Glu Gln Ser Gln Ser Glu Lys Val Arg 385 390 395 400	1200
tta cat tgg cct aca tcc ttg ccc tct gga gat gcc ttt tct tct gtg Leu His Trp Pro Thr Ser Leu Pro Ser Gly Asp Ala Phe Ser Ser Val 405 410 415	1248
ggg aca cat aga ttt gtc caa aag ccc tat agt cgc tct tcc tcc atg Gly Thr His Arg Phe Val Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met 420 425 430	1296
tct tcc att gat cta gtc agt gcc tct gat gat gtt cac aga ttc agc Ser Ser Ile Asp Leu Val Ser Ala Ser Asp Asp Val His Arg Phe Ser 435 440 445	1344
tcc cag gtt gaa gag atg gtg cag aac cac atg act tac tca tta cag Ser Gln Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln 450 455 460	1392
gat gta ggc gga gat gcc aat tgg cag ttg gtt gta gaa gaa gga gaa Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu 465 470 475 480	1440
atg aag gta tac aga aga gaa gta gaa gaa aat ggg att gtt ctg gat Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp 485 490 495	1488
cct tta aaa gct acc cat gca gtt aaa ggc gtc aca gga cat gaa gtc Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val 500 505 510	1536
tgc aat tat ttc tgg aat gtt gac gtt cgc aat gac tgg gaa aca act Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr 515 520 525	1584
ata gaa aac ttt cat gtg gtg gaa aca tta gct gat aat gca atc atc Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile	1632

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530	535	540	
att tat caa aca cac aag agg gtg tgg cct gct tct cag cga gac gta Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val 545 550 555 560			1680
tta tat ctt tct gtc att cga aag ata cca gcc ttg act gaa aat gac Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp 565 570 575			1728
cct gaa act tgg ata gtt tgt aat ttt tct gtg gat cat gac agt gct Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala 580 585 590			1776
cct cta aac aac cga tgt gtc cgt gcc aaa ata aat gtt gct atg att Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile 595 600 605			1824
tgt caa acc ttg gta agc cca cca gag gga aac cag gaa att agc agg Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg 610 615 620			1872
gac aac att cta tgc aag att aca tat gta gct aat gtg aac cct gga Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly 625 630 635 640			1920
gga tgg gca cca gcc tca gtg tta agg gca gtg gca aag cga gag tat Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr 645 650 655			1968
cct aaa ttt cta aaa cgt ttt act tct tac gtc caa gaa aaa act gca Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala 660 665 670			2016
gga aag cct att ttg ttc tag Gly Lys Pro Ile Leu Phe 675			2037

<210> 18
<211> 678
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 18

Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Leu Pro Pro Thr Pro
1 5 10 15

Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
20 25 30

Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu Leu
35 40 45

Leu Gly Cys Arg Ala Ser Met Ser Asp Asn Gln Ser Trp Asn Ser Ser
50 55 60

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Gly Ser Glu Glu Asp Pro Glu Thr Glu Ser Gly Pro Pro Val Glu Arg
65 70 75 80

Cys Gly Val Leu Ser Lys Trp Thr Asn Tyr Ile His Gly Trp Gln Asp
85 90 95

Arg Trp Val Val Leu Lys Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu
100 105 110

Asp Glu Thr Glu Tyr Gly Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala
115 120 125

Val Ile Thr Pro His Asp Phe Asp Glu Cys Arg Phe Asp Ile Ser Val
130 135 140

Asn Asp Ser Val Trp Tyr Leu Arg Ala Gln Asp Pro Asp His Arg Gln
145 150 155 160

Gln Trp Ile Asp Ala Ile Glu Gln His Lys Thr Glu Ser Gly Tyr Gly
165 170 175

Ser Glu Ser Ser Leu Arg Arg His Gly Ser Met Val Ser Leu Val Ser
180 185 190

Gly Ala Ser Gly Tyr Ser Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly
195 200 205

His Ser Leu Arg Glu Lys Leu Ala Glu Met Glu Thr Phe Arg Asp Ile
210 215 220

Leu Cys Arg Gln Val Asp Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala
225 230 235 240

Asp Ala Val Ser Lys Asp Glu Leu Gln Arg Asp Lys Val Val Glu Asp
245 250 255

Asp Glu Asp Asp Phe Pro Thr Thr Arg Ser Asp Gly Asp Phe Leu His
260 265 270

Ser Thr Asn Gly Asn Lys Glu Lys Leu Phe Pro His Val Thr Pro Lys
275 280 285

Gly Ile Asn Gly Ile Asp Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala
290 295 300

Thr Thr Ala Gly Ile Leu Ala Thr Leu Ser His Cys Ile Glu Leu Met
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305	310	315	320
Val Lys Arg Glu Asp Ser Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu			
325	330	335	
Lys Lys Arg Arg Thr Glu Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu			
340	345	350	
Lys Lys Lys Ser His Phe Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn			
355	360	365	
Ser Leu Ile Asn Glu Glu Phe Phe Asp Ala Val Glu Ala Ala Leu			
370	375	380	
Asp Arg Gln Asp Lys Ile Glu Glu Gln Ser Gln Ser Glu Lys Val Arg			
385	390	395	400
Leu His Trp Pro Thr Ser Leu Pro Ser Gly Asp Ala Phe Ser Ser Val			
405	410	415	
Gly Thr His Arg Phe Val Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met			
420	425	430	
Ser Ser Ile Asp Leu Val Ser Ala Ser Asp Asp Val His Arg Phe Ser			
435	440	445	
Ser Gln Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln			
450	455	460	
Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu			
465	470	475	480
Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp			
485	490	495	
Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val			
500	505	510	
Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr			
515	520	525	
Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile			
530	535	540	
Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val			
545	550	555	560

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Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp
565 570 575

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
580 585 590

Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile
595 600 605

Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg
610 615 620

Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly
625 630 635 640

Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
645 650 655

Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala
660 665 670

Gly Lys Pro Ile Leu Phe
675

<210> 19
<211> 1959
<212> DNA
<213> artificial

<220>
<223> Derived sequence

<220>
<221> CDS
<222> (1)..(1959)
<223>

<400> 19
cgg cgc ggc ggg cg₅ act tcg tcc ctc ctc ctg ctc ccc ccc aca ccg
Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Pro Pro Thr Pro
1 5 10 15 48

gag cgg gca ctc ttc gct tcg cca tcc ccc gac cct tca ccc cga gga
Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
20 25 30 96

ctg ggc gcc tcc tcc ggc gca gct gag gga gcg ggg gcc ggt ctc ctg
Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu Leu
35 40 45 144

ctc ggt tgt cga gcc tcc atg tcg gat aat cag agc tgg aac tcg tcg
Leu Gly Cys Arg Ala Ser Met Ser Asp Asn Gln Ser Trp Asn Ser Ser
50 55 60 192

ggc tcg gag gag gat cca gag acg gag tct ggg ccg cct gtg gag cgc
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Gly	Ser	Glu	Glu	Asp	Pro	Glu	Thr	Glu	Ser	Gly	Pro	Pro	Val	Glu	Arg		
65					70				75					80			
tgc	ggg	gtc	ctc	agt	aag	tgg	aca	aac	tac	att	cat	ggg	tgg	cag	gat	288	
Cys	Gly	Val	Leu	Ser	Lys	Trp	Thr	Asn	Tyr	Ile	His	Gly	Trp	Gln	Asp		
														85	90	95	
cgt	tgg	gta	gtt	ttg	aaa	aat	aat	gct	ctg	agt	tac	tac	aaa	tct	gaa	336	
Arg	Trp	Val	Val	Leu	Lys	Asn	Asn	Ala	Leu	Ser	Tyr	Tyr	Lys	Ser	Glu		
														100	105	110	
gat	gaa	aca	gag	tat	ggc	tgc	aga	gga	tcc	atc	tgt	ctt	agc	aag	gct	384	
Asp	Glu	Thr	Glu	Tyr	Gly	Cys	Arg	Gly	Ser	Ile	Cys	Leu	Ser	Lys	Ala		
														115	120	125	
gtc	atc	aca	cct	cac	gat	ttt	gat	gaa	tgt	cga	ttt	gat	att	agt	gta	432	
Val	Ile	Thr	Pro	His	Asp	Phe	Asp	Glu	Cys	Arg	Phe	Asp	Ile	Ser	Val		
														130	135	140	
aat	gat	agt	gtt	tgg	tat	ctt	cgt	gct	cag	gat	cca	gat	cat	aga	cag	480	
Asn	Asp	Ser	Val	Trp	Tyr	Leu	Arg	Ala	Gln	Asp	Pro	Asp	His	Arg	Gln		
														145	150	155	160
caa	tgg	ata	gat	gcc	att	gaa	cag	cac	aag	act	gaa	tct	gga	tat	gga	528	
Gln	Trp	Ile	Asp	Ala	Ile	Glu	Gln	His	Lys	Thr	Glu	Ser	Gly	Tyr	Gly		
														165	170	175	
tct	gaa	tcc	agc	ttg	cgt	cga	cat	ggc	tca	atg	gtg	tcc	ctg	gtg	tct	576	
Ser	Glu	Ser	Ser	Leu	Arg	Arg	His	Gly	Ser	Met	Val	Ser	Leu	Val	Ser		
														180	185	190	
gga	gca	agt	ggc	tac	tct	gca	aca	tcc	acc	tct	tca	ttc	aag	aaa	ggc	624	
Gly	Ala	Ser	Gly	Tyr	Ser	Ala	Thr	Ser	Thr	Ser	Ser	Phe	Lys	Lys	Gly		
														195	200	205	
cac	agt	tta	cgt	gag	aag	ttg	gct	gaa	atg	gaa	aca	ttt	aga	gac	atc	672	
His	Ser	Leu	Arg	Glu	Lys	Leu	Ala	Glu	Met	Glu	Thr	Phe	Arg	Asp	Ile		
														210	215	220	
tta	tgt	aga	caa	gtt	gac	acg	cta	cag	aag	tac	ttt	gat	gcc	tgt	gct	720	
Leu	Cys	Arg	Gln	Val	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	Asp	Ala	Cys	Ala		
														225	230	235	240
gat	gct	gtc	tct	aag	gat	gaa	ctt	caa	agg	gat	aaa	gtg	gta	gaa	gat	768	
Asp	Ala	Val	Ser	Lys	Asp	Glu	Leu	Gln	Arg	Asp	Lys	Val	Val	Glu	Asp		
														245	250	255	
gat	gaa	gat	gac	ttt	cct	aca	acg	cgt	tct	gat	ggt	gac	ttc	ttg	cat	816	
Asp	Glu	Asp	Asp	Phe	Pro	Thr	Thr	Arg	Ser	Asp	Gly	Asp	Phe	Leu	His		
														260	265	270	
agt	acc	aac	ggc	aat	aaa	gaa	aag	tta	ttt	cca	cat	gtg	aca	cca	aaa	864	
Ser	Thr	Asn	Gly	Asn	Lys	Glu	Lys	Leu	Phe	Pro	His	Val	Thr	Pro	Lys		
														275	280	285	
gga	att	aat	ggt	ata	gac	ttt	aaa	ggg	gaa	gcg	ata	act	ttt	aaa	gca	912	
Gly	Ile	Asn	Gly	Ile	Asp	Phe	Lys	Gly	Glu	Ala	Ile	Thr	Phe	Lys	Ala		
														290	295	300	
act	act	gct	gga	atc	ctt	gca	aca	ctt	tct	cat	tgt	att	gaa	cta	atc	960	
Thr	Thr	Ala	Gly	Ile	Leu	Ala	Thr	Leu	Ser	His	Cys	Ile	Glu	Leu	Met		
														305	310	315	320

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gtt	aaa	cgt	gag	gac	agc	tgg	cag	aag	aga	ctg	gat	aag	gaa	act	gag	1008
Val	Lys	Arg	Glu	Asp	Ser	Trp	Gln	Lys	Arg	Leu	Asp	Lys	Glu	Thr	Glu	
325								330					335			
aag	aaa	aga	aga	aca	gag	gaa	gca	tat	aaa	aat	gca	atg	aca	gaa	ctt	1056
Lys	Lys	Arg	Arg	Thr	Glu	Glu	Ala	Tyr	Lys	Asn	Ala	Met	Thr	Glu	Leu	
340				345					350							
aag	aaa	aaa	tcc	cac	ttt	gga	gga	cca	gat	tat	gaa	gaa	ggc	cct	aac	1104
Lys	Lys	Lys	Ser	His	Phe	Gly	Gly	Pro	Asp	Tyr	Glu	Glu	Gly	Pro	Asn	
355						360					365					
agt	ctg	att	aat	gaa	gaa	gag	ttc	ttt	gat	gct	gtt	gaa	gct	gct	ctt	1152
Ser	Leu	Ile	Asn	Glu	Glu	Glu	Phe	Phe	Asp	Ala	Val	Glu	Ala	Ala	Leu	
370				375					380							
gac	aga	caa	gat	aaa	ata	gaa	gaa	cag	tca	cag	agt	gaa	aag	gtg	aga	1200
Asp	Arg	Gln	Asp	Lys	Ile	Glu	Glu	Gln	Ser	Gln	Ser	Glu	Lys	Val	Arg	
385				390				395					400			
tta	cat	tgg	cct	aca	tcc	ttg	ccc	tct	gga	gat	gcc	ttt	tct	tct	gtg	1248
Leu	His	Trp	Pro	Thr	Ser	Leu	Pro	Ser	Gly	Asp	Ala	Phe	Ser	Ser	Val	
						405		410					415			
ggg	aca	cat	aga	ttt	gtc	caa	aag	gtt	gaa	gag	atg	gtg	cag	aac	cac	1296
Gly	Thr	His	Arg	Phe	Val	Gln	Lys	Val	Glu	Glu	Met	Val	Gln	Asn	His	
				420				425				430				
atg	act	tac	tca	tta	cag	gat	gta	ggc	gga	gat	gcc	aat	tgg	cag	ttg	1344
Met	Thr	Tyr	Ser	Leu	Gln	Asp	Val	Gly	Gly	Asp	Ala	Asn	Trp	Gln	Leu	
					435		440				445					
gtt	gta	gaa	gaa	gga	gaa	atg	aag	gta	tac	aga	aga	gaa	gta	gaa	gaa	1392
Val	Val	Glu	Glu	Gly	Glu	Met	Lys	Val	Tyr	Arg	Arg	Glu	Val	Glu	Glu	
					450		455			460						
aat	ggg	att	gtt	ctg	gat	cct	tta	aaa	gct	acc	cat	gca	gtt	aaa	ggc	1440
Asn	Gly	Ile	Val	Leu	Asp	Pro	Leu	Lys	Ala	Thr	His	Ala	Val	Lys	Gly	
					465		470			475			480			
gtc	aca	gga	cat	gaa	gtc	tgc	aat	tat	ttc	tgg	aat	gtt	gac	gtt	cgc	1488
Val	Thr	Gly	His	Glu	Val	Cys	Asn	Tyr	Phe	Trp	Asn	Val	Asp	Val	Arg	
					485			490				495				
aat	gac	tgg	gaa	aca	act	ata	gaa	aac	ttt	cat	gtg	gtg	gaa	aca	tta	1536
Asn	Asp	Trp	Glu	Thr	Thr	Ile	Glu	Asn	Phe	His	Val	Val	Glu	Thr	Leu	
					500			505			510					
gct	gat	aat	gca	atc	atc	att	tat	caa	aca	cac	aag	agg	gtg	tgg	cct	1584
Ala	Asp	Asn	Ala	Ile	Ile	Ile	Tyr	Gln	Thr	His	Lys	Arg	Val	Trp	Pro	
					515		520				525					
gct	tct	cag	cga	gac	gta	tta	tat	ctt	tct	gtc	att	cga	aag	ata	cca	1632
Ala	Ser	Gln	Arg	Asp	Val	Leu	Tyr	Leu	Ser	Val	Ile	Arg	Lys	Ile	Pro	
					530		535			540						
gcc	ttg	act	gaa	aat	gac	cct	gaa	act	tgg	ata	gtt	tgt	aat	ttt	tct	1680
Ala	Leu	Thr	Glu	Asn	Asp	Pro	Glu	Thr	Trp	Ile	Val	Cys	Asn	Phe	Ser	
					545		550			555			560			
gtg	gat	cat	gac	agt	gct	cct	cta	aac	aac	cga	tgt	gtc	cgt	gcc	aaa	1728
Val	Asp	His	Asp	Ser	Ala	Pro	Leu	Asn	Asn	Arg	Cys	Val	Arg	Ala	Lys	
					565			570			575					

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ata aat gtt gct atg att tgt caa acc ttg gta agc cca cca gag gga Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro Pro Glu Gly 580 585 590	1776
aac cag gaa att agc agg gac aac att cta tgc aag att aca tat gta Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val 595 600 605	1824
gct aat gtg aac cct gga gga tgg gca cca gcc tca gtg tta agg gca Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg Ala 610 615 620	1872
gtg gca aag cga gag tat cct aaa ttt cta aaa cgt ttt act tct tac Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr 625 630 635 640	1920
gtc caa gaa aaa act gca gga aag cct att ttg ttc tag Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe 645 650	1959

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<213> artificial

<220>
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<400> 20

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Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
20 25 30

Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu Leu
35 40 45

Leu Gly Cys Arg Ala Ser Met Ser Asp Asn Gln Ser Trp Asn Ser Ser
50 55 60

Gly Ser Glu Glu Asp Pro Glu Thr Glu Ser Gly Pro Pro Val Glu Arg
65 70 75 80

Cys Gly Val Leu Ser Lys Trp Thr Asn Tyr Ile His Gly Trp Gln Asp
85 90 95

Arg Trp Val Val Leu Lys Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu
100 105 110

Asp Glu Thr Glu Tyr Gly Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala
115 120 125

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Val Ile Thr Pro His Asp Phe Asp Glu Cys Arg Phe Asp Ile Ser Val
130 135 140

Asn Asp Ser Val Trp Tyr Leu Arg Ala Gln Asp Pro Asp His Arg Gln
145 150 155 160

Gln Trp Ile Asp Ala Ile Glu Gln His Lys Thr Glu Ser Gly Tyr Gly
165 170 175

Ser Glu Ser Ser Leu Arg Arg His Gly Ser Met Val Ser Leu Val Ser
180 185 190

Gly Ala Ser Gly Tyr Ser Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly
195 200 205

His Ser Leu Arg Glu Lys Leu Ala Glu Met Glu Thr Phe Arg Asp Ile
210 215 220

Leu Cys Arg Gln Val Asp Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala
225 230 235 240

Asp Ala Val Ser Lys Asp Glu Leu Gln Arg Asp Lys Val Val Glu Asp
245 250 255

Asp Glu Asp Asp Phe Pro Thr Thr Arg Ser Asp Gly Asp Phe Leu His
260 265 270

Ser Thr Asn Gly Asn Lys Glu Lys Leu Phe Pro His Val Thr Pro Lys
275 280 285

Gly Ile Asn Gly Ile Asp Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala
290 295 300

Thr Thr Ala Gly Ile Leu Ala Thr Leu Ser His Cys Ile Glu Leu Met
305 310 315 320

Val Lys Arg Glu Asp Ser Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu
325 330 335

Lys Lys Arg Arg Thr Glu Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu
340 345 350

Lys Lys Lys Ser His Phe Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn
355 360 365

Ser Leu Ile Asn Glu Glu Glu Phe Phe Asp Ala Val Glu Ala Ala Leu
370 375 380

Asp Arg Gln Asp Lys Ile Glu Glu Gln Ser Gln Ser Glu Lys Val Arg
 385 390 395 400

Leu His Trp Pro Thr Ser Leu Pro Ser Gly Asp Ala Phe Ser Ser Val
 405 410 415

Gly Thr His Arg Phe Val Gln Lys Val Glu Glu Met Val Gln Asn His
 420 425 430

Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala Asn Trp Gln Leu
 435 440 445

Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg Glu Val Glu Glu
 450 455 460

Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His Ala Val Lys Gly
 465 470 475 480

Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn Val Asp Val Arg
 485 490 495

Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val Val Glu Thr Leu
 500 505 510

Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys Arg Val Trp Pro
 515 520 525

Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro
 530 535 540

Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val Cys Asn Phe Ser
 545 550 555 560

Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys Val Arg Ala Lys
 565 570 575

Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro Pro Glu Gly
 580 585 590

Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val
 595 600 605

Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg Ala
 610 615 620

Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr

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625	630	635	640
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645 650			
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Asp Gly Trp Lys Gly Arg Leu Pro Ser Pro Leu Val Leu Leu Pro Arg			
1	5	10	15
tcc gct cgg tgt cag gcg cgg cgg cgg cgc ggc ggg cgg act tcg tcc 96			
Ser Ala Arg Cys Gln Ala Arg Arg Arg Gly Gly Arg Thr Ser Ser			
20	25	30	
ctc ctc ctg ctc ccc ccc aca ccg gag cgg gca ctc ttc gct tcg cca 144			
Leu Leu Leu Pro Pro Thr Pro Glu Arg Ala Leu Phe Ala Ser Pro			
35	40	45	
tcc ccc gac cct tca ccc cga gga ctg ggc gcc tcc tcc ggc gca gct 192			
Ser Pro Asp Pro Ser Pro Arg Gly Leu Gly Ala Ser Ser Gly Ala Ala			
50	55	60	
gag gga gcg ggg gcc ggt ctc ctg ctc ggt tgt cga gcc tcc atg tcg 240			
Glu Gly Ala Gly Ala Gly Leu Leu Leu Gly Cys Arg Ala Ser Met Ser			
65	70	75	80
gat aat cag agc tgg aac tcg tcg ggc tcg gag gag gat cca gag acg 288			
Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro Glu Thr			
85	90	95	
gag tct ggg ccg cct gtg gag cgc tgc ggg gtc ctc agt aag tgg aca 336			
Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr			
100	105	110	
aac tac att cat ggg tgg cag gat cgt tgg gta gtt ttg aaa aat aat 384			
Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn			
115	120	125	
gct ctg agt tac tac aaa tct gaa gat gaa aca gag tat ggc tgc aga 432			
Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys Arg			
130	135	140	
gga tcc atc tgt ctt agc aag gct gtc atc aca cct cac gat ttt gat 480			
Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp			
145	150	155	160
gaa tgt cga ttt gat att agt gta aat gat agt gtt tgg tat ctt cgt 528			
Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg			

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	165	170	175	
gct cag gat cca gat cat aga cag caa tgg ata gat gcc att gaa cag Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu Gln	180	185	190	576
cac aag act gaa tct gga tat gga tct gaa tcc agc ttg cgt cga cat His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg His	195	200	205	624
ggc tca atg gtg tcc ctg gtg tct gga gca agt ggc tac tct gca aca Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala Thr	210	215	220	672
tcc acc tct tca ttc aag aaa ggc cac agt tta cgt gag aag ttg gct Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu Ala	225	230	235	720
gaa atg gaa aca ttt aga gac atc tta tgt aga caa gtt gac acg cta Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr Leu	245	250	255	768
cag aag tac ttt gat gcc tgt gct gat gct gtc tct aag gat gaa ctt Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu Leu	260	265	270	816
caa agg gat aaa gtg gta gaa gat gat gaa gat gac ttt cct aca acg Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr Thr	275	280	285	864
cgt tct gat ggt gac ttc ttg cat agt acc aac ggc aat aaa gaa aag Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu Lys	290	295	300	912
tta ttt cca cat gtg aca cca aaa gga att aat ggt ata gac ttt aaa Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe Lys	305	310	315	960
ggg gaa gcg ata act ttt aaa gca act act gct gga atc ctt gca aca Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala Thr	325	330	335	1008
ctt tct cat tgt att gaa cta atg gtt aaa cgt gag gac agc tgg cag Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp Gln	340	345	350	1056
aag aga ctg gat aag gaa act gag aag aaa aga aga aca gag gaa gca Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu Ala	355	360	365	1104
tat aaa aat gca atg aca gaa ctt aag aaa aaa tcc cac ttt gga gga Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Ser His Phe Gly Gly	370	375	380	1152
cca gat tat gaa gaa ggc cct aac agt ctg att aat gaa gaa gag ttc Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu Phe	385	390	395	1200
ttt gat gct gtt gaa gct gct ctt gac aga caa gat aaa ata gaa gaa Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu Glu	405	410	415	1248
cag tca cag agt gaa aag gtg aga tta cat tgg cct aca tcc ttg ccc				1296

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Gln	Ser	Gln	Ser	Glu	Lys	Val	Arg	Leu	His	Trp	Pro	Thr	Ser	Leu	Pro
420				425								430			
tct	gga	gat	gcc	ttt	tct	tct	gtg	ggg	aca	cat	aga	ttt	gtc	caa	aag
Ser	Gly	Asp	Ala	Phe	Ser	Ser	Val	Gly	Thr	His	Arg	Phe	Val	Gln	Lys
435				440								445			
ccc	tat	agt	cgc	tct	tcc	tcc	atg	tct	tcc	att	gat	cta	gtc	agt	gcc
Pro	Tyr	Ser	Arg	Ser	Ser	Ser	Met	Ser	Ser	Ile	Asp	Leu	Val	Ser	Ala
450				455							460				
tct	gat	gat	gtt	cac	aga	ttc	agc	tcc	cag	gtt	gaa	gag	atg	gtg	cag
Ser	Asp	Asp	Val	His	Arg	Phe	Ser	Ser	Gln	Val	Glu	Glu	Met	Val	Gln
465				470					475				480		
aac	cac	atg	act	tac	tca	tta	cag	gat	gta	ggc	gga	gat	gcc	aat	tgg
Asn	His	Met	Thr	Tyr	Ser	Leu	Gln	Asp	Val	Gly	Gly	Asp	Ala	Asn	Trp
485								490				495			
cag	ttg	gtt	gta	gaa	gaa	gga	gaa	atg	aag	gta	tac	aga	aga	gaa	gta
Gln	Leu	Val	Val	Glu	Glu	Gly	Glu	Met	Lys	Val	Tyr	Arg	Arg	Glu	Val
500								505				510			
gaa	gaa	aat	ggg	att	gtt	ctg	gat	cct	tta	aaa	gct	acc	cat	gca	gtt
Glu	Glu	Asn	Gly	Ile	Val	Leu	Asp	Pro	Leu	Lys	Ala	Thr	His	Ala	Val
515							520				525				
aaa	ggc	gtc	aca	gga	cat	gaa	gtc	tgc	aat	tat	ttc	tgg	aat	gtt	gac
Lys	Gly	Val	Thr	Gly	His	Glu	Val	Cys	Asn	Tyr	Phe	Trp	Asn	Val	Asp
530						535				540					
gtt	cgc	aat	gac	tgg	gaa	aca	act	ata	gaa	aac	ttt	cat	gtg	gtg	gaa
Val	Arg	Asn	Asp	Trp	Glu	Thr	Thr	Ile	Glu	Asn	Phe	His	Val	Val	Glu
545					550				555				560		
aca	tta	gct	gat	aat	gca	atc	atc	att	tat	caa	aca	cac	aag	agg	gtg
Thr	Leu	Ala	Asp	Asn	Ala	Ile	Ile	Ile	Tyr	Gln	Thr	His	Lys	Arg	Val
565								570				575			
tgg	cct	gct	tct	cag	cga	gac	gta	tta	tat	ctt	tct	gtc	att	cga	aag
Trp	Pro	Ala	Ser	Gln	Arg	Asp	Val	Leu	Tyr	Leu	Ser	Val	Ile	Arg	Lys
580							585					590			
ata	cca	gcc	ttg	act	gaa	aat	gac	cct	gaa	act	tgg	ata	gtt	tgt	aat
Ile	Pro	Ala	Leu	Thr	Glu	Asn	Asp	Pro	Glu	Thr	Trp	Ile	Val	Cys	Asn
595							600				605				
ttt	tct	gtg	gat	cat	gac	agt	gct	cct	cta	aac	aac	cga	tgt	gtc	cgt
Phe	Ser	Val	Asp	His	Asp	Ser	Ala	Pro	Leu	Asn	Asn	Arg	Cys	Val	Arg
610					615						620				
gcc	aaa	ata	aat	gtt	gct	atg	att	tgt	caa	acc	ttg	gta	agc	cca	cca
Ala	Lys	Ile	Asn	Val	Ala	Met	Ile	Cys	Gln	Thr	Leu	Val	Ser	Pro	Pro
625					630				635				640		
gag	gga	aac	cag	gaa	att	agc	agg	gac	aac	att	cta	tgc	aag	att	aca
Glu	Gly	Asn	Gln	Glu	Ile	Ser	Arg	Asp	Asn	Ile	Leu	Cys	Lys	Ile	Thr
645								650				655			
tat	gta	gct	aat	gtg	aac	cct	gga	gga	tgg	gca	cca	gcc	tca	gtg	tta
Tyr	Val	Ala	Asn	Val	Asn	Pro	Gly	Gly	Trp	Ala	Pro	Ala	Ser	Val	Leu
660					665						670				

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agg gca gtg gca aag cga gag tat cct aaa ttt cta aaa cgt ttt act	2064
Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr	
675 680 685	
tct tac gtc caa gaa aaa act gca gga aag cct att ttg ttc tag	2109
Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe	
690 695 700	
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35 40 45	
Ser Pro Asp Pro Ser Pro Arg Gly Leu Gly Ala Ser Ser Gly Ala Ala	
50 55 60	
Glu Gly Ala Gly Ala Gly Leu Leu Leu Gly Cys Arg Ala Ser Met Ser	
65 70 75 80	
Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro Glu Thr	
85 90 95	
Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr	
100 105 110	
Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn	
115 120 125	
Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys Arg	
130 135 140	
Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp	
145 150 155 160	
Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg	
165 170 175	

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Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu Gln
180 185 190

His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg His
195 200 205

Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala Thr
210 215 220

Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu Ala
225 230 235 240

Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr Leu
245 250 255

Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu Leu
260 265 270

Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr Thr
275 280 285

Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu Lys
290 295 300

Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe Lys
305 310 315 320

Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala Thr
325 330 335

Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp Gln
340 345 350

Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu Ala
355 360 365

Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Ser His Phe Gly Gly
370 375 380

Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu Phe
385 390 395 400

Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu Glu
405 410 415

Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu Pro
420 425 430

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Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln Lys
435 440 445

Pro Tyr Ser Arg Ser Ser Met Ser Ser Ile Asp Leu Val Ser Ala
450 455 460

Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met Val Gln
465 470 475 480

Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala Asn Trp
485 490 495

Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg Glu Val
500 505 510

Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His Ala Val
515 520 525

Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn Val Asp
530 535 540

Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val Val Glu
545 550 555 560

Thr Leu Ala Asp Asn Ala Ile Ile Tyr Gln Thr His Lys Arg Val
565 570 575

Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile Arg Lys
580 585 590

Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val Cys Asn
595 600 605

Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys Val Arg
610 615 620

Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro Pro
625 630 635 640

Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr
645 650 655

Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu
660 665 670

Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr
675 680 685

Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
 690 695 700

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Asp Gly Trp Lys Gly Arg Leu Pro Ser Pro Leu Val Leu Leu Pro Arg		
1 5 10 15		
tcc gct cgg tgt cag gcg cgg cgg cgc ggc ggg cgg act tcg tcc		96
Ser Ala Arg Cys Gln Ala Arg Arg Arg Gly Gly Arg Thr Ser Ser		
20 25 30		
ctc ctc ctg ctc ccc ccc aca ccg gag cgg gca ctc ttc gct tcg cca		144
Leu Leu Leu Pro Pro Thr Pro Glu Arg Ala Leu Phe Ala Ser Pro		
35 40 45		
tcc ccc gac cct tca ccc cga gga ctg ggc gcc tcc tcc ggc gca gct		192
Ser Pro Asp Pro Ser Pro Arg Gly Leu Gly Ala Ser Ser Gly Ala Ala		
50 55 60		
gag gga gcg ggg gcc ggt ctc ctg ctc ggt tgt cga gcc tcc atg tcg		240
Glu Gly Ala Gly Ala Gly Leu Leu Gly Cys Arg Ala Ser Met Ser		
65 70 75 80		
gat aat cag agc tgg aac tcg tcg ggc tcg gag gag gat cca gag acg		288
Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro Glu Thr		
85 90 95		
gag tct ggg ccg cct gtg gag cgc tgc ggg gtc ctc agt aag tgg aca		336
Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr		
100 105 110		
aac tac att cat ggg tgg cag gat cgt tgg gta gtt ttg aaa aat aat		384
Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn		
115 120 125		
gct ctg agt tac tac aaa tct gaa gat gaa aca gag tat ggc tgc aga		432
Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys Arg		
130 135 140		
gga tcc atc tgt ctt agc aag gct gtc atc aca cct cac gat ttt gat		480
Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp		
145 150 155 160		
gaa tgt cga ttt gat att agt gta aat gat agt gtt tgg tat ctt cgt		528
Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg		
165 170 175		

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gct cag gat cca gat cat aga cag caa tgg ata gat gcc att gaa cag	576
Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu Gln	
180 185 190	
cac aag act gaa tct gga tat gga tct gaa tcc agc ttg cgt cga cat	624
His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg His	
195 200 205	
ggc tca atg gtg tcc ctg gtg tct gga gca agt ggc tac tct gca aca	672
Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala Thr	
210 215 220	
tcc acc tct tca ttc aag aaa ggc cac agt tta cgt gag aag ttg gct	720
Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu Ala	
225 230 235 240	
gaa atg gaa aca ttt aga gac atc tta tgt aga caa gtt gac acg cta	768
Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr Leu	
245 250 255	
cag aag tac ttt gat gcc tgt gct gat gct gtc tct aag gat gaa ctt	816
Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu Leu	
260 265 270	
caa agg gat aaa gtg gta gaa gat gat gaa gat gac ttt cct aca acg	864
Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr Thr	
275 280 285	
cgt tct gat ggt gac ttc ttg cat agt acc aac ggc aat aaa gaa aag	912
Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu Lys	
290 295 300	
tta ttt cca cat gtg aca cca aaa gga att aat ggt ata gac ttt aaa	960
Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe Lys	
305 310 315 320	
ggg gaa gcg ata act ttt aaa gca act act gct gga atc ctt gca aca	1008
Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala Thr	
325 330 335	
ctt tct cat tgt att gaa cta atg gtt aaa cgt gag gac agc tgg cag	1056
Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp Gln	
340 345 350	
aag aga ctg gat aag gaa act gag aag aaa aga aga aca gag gaa gca	1104
Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu Ala	
355 360 365	
tat aaa aat gca atg aca gaa ctt aag aaa aaa tcc cac ttt gga gga	1152
Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Ser His Phe Gly Gly	
370 375 380	
cca gat tat gaa gaa ggc cct aac agt ctg att aat gaa gaa gag ttc	1200
Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu Phe	
385 390 395 400	
ttt gat gct gtt gaa gct gct ctt gac aga caa gat aaa ata gaa gaa	1248
Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu Glu	
405 410 415	
cag tca cag agt gaa aag gtg aga tta cat tgg cct aca tcc ttg ccc	1296
Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu Pro	

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420	425	430	1344										
tct gga gat gcc ttt tct tct gtg ggg aca cat aga ttt gtc caa aag													
Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln Lys													
435	440	445											
gtt gaa gag atg gtg cag aac cac atg act tac tca tta cag gat gta													
Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val													
450	455	460											
ggc gga gat gcc aat tgg cag ttg gtt gta gaa gaa gga gaa atg aag													
Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys													
465	470	475											
gta tac aga aga gaa gta gaa gaa aat ggg att gtt ctg gat cct tta													
Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu													
485	490	495											
aaa gct acc cat gca gtt aaa ggc gtc aca gga cat gaa gtc tgc aat													
Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn													
500	505	510											
tat ttc tgg aat gtt gac gtt cgc aat gac tgg gaa aca act ata gaa													
Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu													
515	520	525											
aac ttt cat gtg gtg gaa aca tta gct gat aat gca atc atc att tat													
Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr													
530	535	540											
caa aca cac aag agg gtg tgg cct gct tct cag cga gac gta tta tat													
Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr													
545	550	555											
ctt tct gtc att cga aag ata cca gcc ttg act gaa aat gac cct gaa													
Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu													
565	570	575											
act tgg ata gtt tgt aat ttt tct gtg gat cat gac agt gct cct cta													
Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu													
580	585	590											
aac aac cga tgt gtc cgt gcc aaa ata aat gtt gct atg att tgt caa													
Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln													
595	600	605											
acc ttg gta agc cca cca gag gga aac cag gaa att agc agg gac aac													
Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn													
610	615	620											
att cta tgc aag att aca tat gta gct aat gtg aac cct gga gga tgg													
Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp													
625	630	635											
640													
gca cca gcc tca gtg tta agg gca gtg gca aag cga gag tat cct aaa													
Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys													
645	650	655											
ttt cta aaa cgt ttt act tct tac gtc caa gaa aaa act gca gga aag													
Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gln Lys													
660	665	670											
cct att ttg ttc tag													
			2031										

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Pro Ile Leu Phe
675

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<211> 676
<212> PRT
<213> artificial

<220>
<223> Derived sequence

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Ser Ala Arg Cys Gln Ala Arg Arg Arg Gly Gly Arg Thr Ser Ser
20 25 30

Leu Leu Leu Leu Pro Pro Thr Pro Glu Arg Ala Leu Phe Ala Ser Pro
35 40 45

Ser Pro Asp Pro Ser Pro Arg Gly Leu Gly Ala Ser Ser Gly Ala Ala
50 55 60

Glu Gly Ala Gly Ala Gly Leu Leu Leu Gly Cys Arg Ala Ser Met Ser
65 70 75 80

Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro Glu Thr
85 90 95

Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr
100 105 110

Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn
115 120 125

Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys Arg
130 135 140

Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp
145 150 155 160

Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg
165 170 175

Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu Gln
180 185 190

His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg His
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195

200

205

Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala Thr
210 215 220

Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu Ala
225 230 235 240

Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr Leu
245 250 255

Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu Leu
260 265 270

Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr Thr
275 280 285

Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys Glu Lys
290 295 300

Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe Lys
305 310 315 320

Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala Thr
325 330 335

Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp Gln
340 345 350

Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu Glu Ala
355 360 365

Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Ser His Phe Gly Gly
370 375 380

Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu Phe
385 390 395 400

Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu Glu
405 410 415

Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu Pro
420 425 430

Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln Lys
435 440 445

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Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val
450 455 460

Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys
465 470 475 480

Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu
485 490 495

Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn
500 505 510

Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu
515 520 525

Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr
530 535 540

Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr
545 550 555 560

Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu
565 570 575

Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu
580 585 590

Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln
595 600 605

Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn
610 615 620

Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp
625 630 635 640

Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys
645 650 655

Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys
660 665 670

Pro Ile Leu Phe
675

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03-075-US

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<222> (1)..(2181)

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1				5				10				15				

gtc	acg	gcf	acg	gcf	gcf	gcf	gct	gac	ggc	tgg	aag	ggt	agg	ctt	cct	96
Val	Thr	Ala	Thr	Ala	Ala	Ala	Ala	Asp	Gly	Trp	Lys	Gly	Arg	Leu	Pro	
				20				25			30					

tca	ccg	ctc	gtc	ctc	ctt	cct	cgc	tcc	gct	cgf	tgt	cag	gcf	cgg	cgg	144
Ser	Pro	Leu	Val	Leu	Leu	Pro	Arg	Ser	Ala	Arg	Cys	Gln	Ala	Arg	Arg	
				35			40				45					

cgg	cgc	ggc	ggg	cgg	act	tcg	tcc	ctc	ctc	ctg	ctc	ccc	ccc	aca	ccg	192
Arg	Arg	Gly	Gly	Arg	Thr	Ser	Ser	Leu	Leu	Leu	Leu	Pro	Pro	Thr	Pro	
				50			55				60					

gag	cgg	gca	ctc	tcc	gct	tcg	cca	tcc	ccc	gac	cct	tca	ccc	cga	gga	240
Glu	Arg	Ala	Leu	Phe	Ala	Ser	Pro	Ser	Pro	Asp	Pro	Ser	Pro	Arg	Gly	
				65			70			75				80		

ctg	ggc	gcc	tcc	tcc	ggc	gca	gct	gag	gga	gcf	ggg	gcc	ggt	ctc	ctg	288
Leu	Gly	Ala	Ser	Ser	Gly	Ala	Ala	Glu	Gly	Ala	Gly	Ala	Gly	Leu	Leu	
				85			90			95						

ctc	ggf	tgt	cga	gcc	tcc	atg	tcg	gat	aat	cag	agc	tgg	aac	tcg	tcg	336
Leu	Gly	Cys	Arg	Ala	Ser	Met	Ser	Asp	Asn	Gln	Ser	Trp	Asn	Ser	Ser	
				100			105				110					

ggc	tcg	gag	gag	gat	cca	gag	acg	gag	tct	ggg	ccg	cct	gtg	gag	cgc	384
Gly	Ser	Glu	Glu	Asp	Pro	Glu	Thr	Glu	Ser	Gly	Pro	Pro	Val	Glu	Arg	
				115			120			125						

tgc	ggg	gtc	ctc	agt	aag	tgg	aca	aac	tac	att	cat	ggg	tgg	cag	gat	432
Cys	Gly	Val	Leu	Ser	Lys	Trp	Thr	Asn	Tyr	Ile	His	Gly	Trp	Gln	Asp	
				130			135			140						

cgt	tgg	gta	gtt	ttg	aaa	aat	aat	gct	ctg	agt	tac	tac	aaa	tct	gaa	480
Arg	Trp	Val	Val	Leu	Lys	Asn	Asn	Ala	Leu	Ser	Tyr	Tyr	Lys	Ser	Glu	
				145			150			155			160			

gat	gaa	aca	gag	tat	ggc	tgc	aga	gga	tcc	atc	tgt	ctt	agc	aag	gct	528
Asp	Glu	Thr	Glu	Tyr	Gly	Cys	Arg	Gly	Ser	Ile	Cys	Leu	Ser	Lys	Ala	
				165			170			175						

gtc	atc	aca	cct	cac	gat	ttt	gat	gaa	tgt	cga	ttt	gat	att	agt	gta	576
Val	Ile	Thr	Pro	His	Asp	Phe	Asp	Glu	Cys	Arg	Phe	Asp	Ile	Ser	Val	
				180			185			190						

aat	gat	agt	gtt	tgg	tat	ctt	cgt	gct	cag	gat	cca	gat	cat	aga	cag	624
Asn	Asp	Ser	Val	Trp	Tyr	Leu	Arg	Ala	Gln	Asp	Pro	Asp	His	Arg	Gln	
				195			200			205						

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caa	tgg	ata	gat	gcc	att	gaa	cag	cac	aag	act	gaa	tct	gga	tat	gga	672
Gln	Trp	Ile	Asp	Ala	Ile	Glu	Gln	His	Lys	Thr	Glu	Ser	Gly	Tyr	Gly	
210					215					220						
tct	gaa	tcc	agc	ttg	cgt	cga	cat	ggc	tca	atg	gtg	tcc	ctg	gtg	tct	720
Ser	Glu	Ser	Ser	Leu	Arg	Arg	His	Gly	Ser	Met	Val	Ser	Leu	Val	Ser	
225				230					235				240			
gga	gca	agt	ggc	tac	tct	gca	aca	tcc	acc	tct	tca	ttc	aag	aaa	ggc	768
Gly	Ala	Ser	Gly	Tyr	Ser	Ala	Thr	Ser	Thr	Ser	Ser	Phe	Lys	Lys	Gly	
				245					250				255			
cac	agt	tta	cgt	gag	aag	ttg	gct	gaa	atg	gaa	aca	ttt	aga	gac	atc	816
His	Ser	Leu	Arg	Glu	Lys	Leu	Ala	Glu	Met	Glu	Thr	Phe	Arg	Asp	Ile	
				260				265				270				
tta	tgt	aga	caa	gtt	gac	acg	cta	cag	aag	tac	ttt	gat	gcc	tgt	gct	864
Leu	Cys	Arg	Gln	Val	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	Asp	Ala	Cys	Ala	
				275				280				285				
gat	gct	gtc	tct	aag	gat	gaa	ctt	caa	agg	gat	aaa	gtg	gta	gaa	gat	912
Asp	Ala	Val	Ser	Lys	Asp	Glu	Leu	Gln	Arg	Asp	Lys	Val	Val	Glu	Asp	
				290				295				300				
gat	gaa	gat	gac	ttt	cct	aca	acg	cgt	tct	gat	ggt	gac	ttc	ttg	cat	960
Asp	Glu	Asp	Asp	Phe	Pro	Thr	Thr	Arg	Ser	Asp	Gly	Asp	Phe	Leu	His	
				305				310				315				
agt	acc	aac	ggc	aat	aaa	gaa	aag	tta	ttt	cca	cat	gtg	aca	cca	aaa	1008
Ser	Thr	Asn	Gly	Asn	Lys	Glu	Lys	Leu	Phe	Pro	His	Val	Thr	Pro	Lys	
				325					330				335			
gga	att	aat	ggt	ata	gac	ttt	aaa	ggg	gaa	gcg	ata	act	ttt	aaa	gca	1056
Gly	Ile	Asn	Gly	Ile	Asp	Phe	Lys	Gly	Glu	Ala	Ile	Thr	Phe	Lys	Ala	
				340				345				350				
act	act	gct	gga	atc	ctt	gca	aca	ctt	tct	cat	tgt	att	gaa	cta	atg	1104
Thr	Thr	Ala	Gly	Ile	Leu	Ala	Thr	Leu	Ser	His	Cys	Ile	Glu	Leu	Met	
				355				360				365				
gtt	aaa	cgt	gag	gac	agc	tgg	cag	aag	aga	ctg	gat	aag	gaa	act	gag	1152
Val	Lys	Arg	Glu	Asp	Ser	Trp	Gln	Lys	Arg	Leu	Asp	Lys	Glu	Thr	Glu	
				370				375				380				
aag	aaa	aga	aga	aca	gag	gaa	gca	tat	aaa	aat	gca	atg	aca	gaa	ctt	1200
Lys	Lys	Arg	Arg	Thr	Glu	Glu	Ala	Tyr	Lys	Asn	Ala	Met	Thr	Glu	Leu	
				385				390				395				
aag	aaa	aaa	tcc	cac	ttt	gga	gga	cca	gat	tat	gaa	gaa	ggc	cct	aac	1248
Lys	Lys	Lys	Ser	His	Phe	Gly	Gly	Pro	Asp	Tyr	Glu	Glu	Gly	Pro	Asn	
				405				410				415				
agt	ctg	att	aat	gaa	gaa	gag	ttc	ttt	gat	gct	gtt	gaa	gct	gct	ctt	1296
Ser	Leu	Ile	Asn	Glu	Glu	Phe	Phe	Asp	Ala	Val	Glu	Ala	Ala	Leu		
				420				425				430				
gac	aga	caa	gat	aaa	ata	gaa	gaa	cag	tca	cag	agt	gaa	aag	gtg	aga	1344
Asp	Arg	Gln	Asp	Lys	Ile	Glu	Glu	Gln	Ser	Gln	Ser	Glu	Lys	Val	Arg	
				435				440				445				
tta	cat	tgg	cct	aca	tcc	ttg	ccc	tct	gga	gat	gcc	ttt	tct	tct	gtg	1392
Leu	His	Trp	Pro	Thr	Ser	Leu	Pro	Ser	Gly	Asp	Ala	Phe	Ser	Ser	Val	
				450				455				460				

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ggg aca cat aga ttt gtc caa aag ccc tat agt cgc tct tcc tcc atg Gly Thr His Arg Phe Val Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met 465 470 475 480	1440
tct tcc att gat cta gtc agt gcc tct gat gat gtt cac aga ttc agc Ser Ser Ile Asp Leu Val Ser Ala Ser Asp Asp Val His Arg Phe Ser 485 490 495	1488
tcc cag gtt gaa gag atg gtc cag aac cac atg act tac tca tta cag Ser Gln Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln 500 505 510	1536
gat gta ggc gga gat gcc aat tgg cag ttg gtt gta gaa gaa gga gaa Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu 515 520 525	1584
atg aag gta tac aga aga gaa gta gaa gaa aat ggg att gtt ctg gat Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp 530 535 540	1632
cct tta aaa gct acc cat gca gtt aaa ggc gtc aca gga cat gaa gtc Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val 545 550 555 560	1680
tgc aat tat ttc tgg aat gtt gac gtt cgc aat gac tgg gaa aca act Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr 565 570 575	1728
ata gaa aac ttt cat gtg gtg gaa aca tta gct gat aat gca atc atc Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile 580 585 590	1776
att tat caa aca cac aag agg gtg tgg cct gct tct cag cga gac gta Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val 595 600 605	1824
tta tat ctt tct gtc att cga aag ata cca gcc ttg act gaa aat gac Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp 610 615 620	1872
cct gaa act tgg ata gtt tgt aat ttt tct gtg gat cat gac agt gct Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala 625 630 635 640	1920
cct cta aac aac cga tgt gtc cgt gcc aaa ata aat gtt gct atg att Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile 645 650 655	1968
tgt caa acc ttg gta agc cca cca gag gga aac cag gaa att agc agg Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg 660 665 670	2016
gac aac att cta tgc aag att aca tat gta gct aat gtg aac cct gga Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly 675 680 685	2064
gga tgg gca cca gcc tca gtg tta agg gca gtg gca aag cga gag tat Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr 690 695 700	2112
cct aaa ttt cta aaa cgt ttt act tct tac gtc caa gaa aaa act gca Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala	2160

705

710

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715

720

gga aag cct att ttg ttc tag
Gly Lys Pro Ile Leu Phe
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2181

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<223> Derived sequence

<400> 26

Ala Ser Arg Gly Leu Ser Ser Gly Gly Ser Ala Gly Arg Asn Ala Gly
1 5 10 15

Val Thr Ala Thr Ala Ala Ala Ala Asp Gly Trp Lys Gly Arg Leu Pro
20 25 30

Ser Pro Leu Val Leu Leu Pro Arg Ser Ala Arg Cys Gln Ala Arg Arg
35 40 45

Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Leu Pro Pro Thr Pro
50 55 60

Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
65 70 75 80

Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu Leu
85 90 95

Leu Gly Cys Arg Ala Ser Met Ser Asp Asn Gln Ser Trp Asn Ser Ser
100 105 110

Gly Ser Glu Glu Asp Pro Glu Thr Glu Ser Gly Pro Pro Val Glu Arg
115 120 125

Cys Gly Val Leu Ser Lys Trp Thr Asn Tyr Ile His Gly Trp Gln Asp
130 135 140

Arg Trp Val Val Leu Lys Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu
145 150 155 160

Asp Glu Thr Glu Tyr Gly Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala
165 170 175

Val Ile Thr Pro His Asp Phe Asp Glu Cys Arg Phe Asp Ile Ser Val
180 185 190

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Asn Asp Ser Val Trp Tyr Leu Arg Ala Gln Asp Pro Asp His Arg Gln
195 200 205

Gln Trp Ile Asp Ala Ile Glu Gln His Lys Thr Glu Ser Gly Tyr Gly
210 215 220

Ser Glu Ser Ser Leu Arg Arg His Gly Ser Met Val Ser Leu Val Ser
225 230 235 240

Gly Ala Ser Gly Tyr Ser Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly
245 250 255

His Ser Leu Arg Glu Lys Leu Ala Glu Met Glu Thr Phe Arg Asp Ile
260 265 270

Leu Cys Arg Gln Val Asp Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala
275 280 285

Asp Ala Val Ser Lys Asp Glu Leu Gln Arg Asp Lys Val Val Glu Asp
290 295 300

Asp Glu Asp Asp Phe Pro Thr Thr Arg Ser Asp Gly Asp Phe Leu His
305 310 315 320

Ser Thr Asn Gly Asn Lys Glu Lys Leu Phe Pro His Val Thr Pro Lys
325 330 335

Gly Ile Asn Gly Ile Asp Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala
340 345 350

Thr Thr Ala Gly Ile Leu Ala Thr Leu Ser His Cys Ile Glu Leu Met
355 360 365

Val Lys Arg Glu Asp Ser Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu
370 375 380

Lys Lys Arg Arg Thr Glu Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu
385 390 395 400

Lys Lys Lys Ser His Phe Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn
405 410 415

Ser Leu Ile Asn Glu Glu Glu Phe Phe Asp Ala Val Glu Ala Ala Leu
420 425 430

Asp Arg Gln Asp Lys Ile Glu Glu Gln Ser Gln Ser Glu Lys Val Arg
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435

440

445

Leu His Trp Pro Thr Ser Leu Pro Ser Gly Asp Ala Phe Ser Ser Val
450 455 460

Gly Thr His Arg Phe Val Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met
465 470 475 480

Ser Ser Ile Asp Leu Val Ser Ala Ser Asp Asp Val His Arg Phe Ser
485 490 495

Ser Gln Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln
500 505 510

Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu
515 520 525

Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp
530 535 540

Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val
545 550 555 560

Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr
565 570 575

Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile
580 585 590

Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val
595 600 605

Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp
610 615 620

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
625 630 635 640

Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile
645 650 655

Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg
660 665 670

Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly
675 680 685

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Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
690 695 700 705

Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala
705 710 715 720

Gly Lys Pro Ile Leu Phe
725

<210> 27
<211> 2103
<212> DNA
<213> artificial

<220>
<223> Derived sequence

<220>
<221> CDS
<222> (1)..(2103)
<223>

<400> 27
gca tcg agg ggg cta agt tcg ggt ggc agc gcc ggg cgc aac gca ggg 48
Ala Ser Arg Gly Leu Ser Ser Gly Gly Ser Ala Gly Arg Asn Ala Gly
1 5 10 15

gtc acg gcg acg gcg gcg gct gac ggc tgg aag ggt agg ctt cct 96
Val Thr Ala Thr Ala Ala Ala Asp Gly Trp Lys Gly Arg Leu Pro
20 25 30

tca ccg ctc gtc ctc ctt cct cgc tcc gct cgg tgt cag gcg cgg cgg 144
Ser Pro Leu Val Leu Pro Arg Ser Ala Arg Cys Gln Ala Arg Arg
35 40 45

cgg cgc ggc ggg cgg act tcg tcc ctc ctc ctg ctc ccc ccc aca ccg 192
Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Pro Pro Thr Pro
50 55 60

gag cgg gca ctc ttc gct tcg cca tcc ccc gac cct tca ccc cga gga 240
Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
65 70 75 80

ctg ggc gcc tcc tcc ggc gca gct gag gga gcg ggg gcc ggt ctc ctg 288
Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu Leu
85 90 95

ctc ggt tgt cga gcc tcc atg tcg gat aat cag agc tgg aac tcg tcg 336
Leu Gly Cys Arg Ala Ser Met Ser Asp Asn Gln Ser Trp Asn Ser Ser
100 105 110

ggc tcg gag gag gat cca gag acg gag tct ggg ccg cct gtg gag cgc 384
Gly Ser Glu Glu Asp Pro Glu Thr Glu Ser Gly Pro Pro Val Glu Arg
115 120 125

tgc ggg gtc ctc agt aag tgg aca aac tac att cat ggg tgg cag gat 432
Cys Gly Val Leu Ser Lys Trp Thr Asn Tyr Ile His Gly Trp Gln Asp
130 135 140

cgt tgg gta gtt ttg aaa aat aat gct ctg agt tac tac aaa tct gaa 480

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Arg	Trp	Val	Val	Leu	Lys	Asn	Asn	Ala	Leu	Ser	Tyr	Tyr	Lys	Ser	Glu	
145				150					155					160		
gat	gaa	aca	gag	tat	ggc	tgc	aga	gga	tcc	atc	tgt	ctt	agc	aag	gct	528
Asp	Glu	Thr	Glu	Tyr	Gly	Cys	Arg	Gly	Ser	Ile	Cys	Leu	Ser	Lys	Ala	
				165					170					175		
gtc	atc	aca	cct	cac	gat	ttt	gat	gaa	tgt	cga	ttt	gat	att	agt	gta	576
Val	Ile	Thr	Pro	His	Asp	Phe	Asp	Glu	Cys	Arg	Phe	Asp	Ile	Ser	Val	
				180				185					190			
aat	gat	agt	gtt	tgg	tat	ctt	cgt	gct	cag	gat	cca	gat	cat	aga	cag	624
Asn	Asp	Ser	Val	Trp	Tyr	Leu	Arg	Ala	Gln	Asp	Pro	Asp	His	Arg	Gln	
				195				200					205			
caa	tgg	ata	gat	gcc	att	gaa	cag	cac	aag	act	gaa	tct	gga	tat	gga	672
Gln	Trp	Ile	Asp	Ala	Ile	Glu	Gln	His	Lys	Thr	Glu	Ser	Gly	Tyr	Gly	
				210			215				220					
tct	gaa	tcc	agc	ttg	cgt	cga	cat	ggc	tca	atg	gtg	tcc	ctg	gtg	tct	720
Ser	Glu	Ser	Ser	Leu	Arg	Arg	His	Gly	Ser	Met	Val	Ser	Leu	Val	Ser	
				225			230				235				240	
gga	gca	agt	ggc	tac	tct	gca	aca	tcc	acc	tct	tca	ttc	aag	aaa	ggc	768
Gly	Ala	Ser	Gly	Tyr	Ser	Ala	Thr	Ser	Thr	Ser	Ser	Phe	Lys	Lys	Gly	
				245			250						255			
cac	agt	tta	cgt	gag	aag	ttg	gct	gaa	atg	gaa	aca	ttt	aga	gac	atc	816
His	Ser	Leu	Arg	Glu	Lys	Leu	Ala	Glu	Met	Glu	Thr	Phe	Arg	Asp	Ile	
				260			265				270					
tta	tgt	aga	caa	gtt	gac	acg	cta	cag	aag	tac	ttt	gat	gcc	tgt	gct	864
Leu	Cys	Arg	Gln	Val	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	Asp	Ala	Cys	Ala	
				275			280				285					
gat	gct	gtc	tct	aag	gat	gaa	ctt	caa	agg	gat	aaa	gtg	gta	gaa	gat	912
Asp	Ala	Val	Ser	Lys	Asp	Glu	Leu	Gln	Arg	Asp	Lys	Val	Val	Glu	Asp	
				290			295				300					
gat	gaa	gat	gac	ttt	cct	aca	acg	cgt	tct	gat	ggt	gac	ttc	ttg	cat	960
Asp	Glu	Asp	Asp	Phe	Pro	Thr	Thr	Arg	Ser	Asp	Gly	Asp	Phe	Leu	His	
				305			310				315				320	
agt	acc	aac	ggc	aat	aaa	gaa	aag	tta	ttt	cca	cat	gtg	aca	cca	aaa	1008
Ser	Thr	Asn	Gly	Asn	Lys	Glu	Lys	Leu	Phe	Pro	His	Val	Thr	Pro	Lys	
				325			330						335			
gga	att	aat	ggt	ata	gac	ttt	aaa	ggg	gaa	gcg	ata	act	ttt	aaa	gca	1056
Gly	Ile	Asn	Gly	Ile	Asp	Phe	Lys	Gly	Glu	Ala	Ile	Thr	Phe	Lys	Ala	
				340			345				350					
act	act	gct	gga	atc	ctt	gca	aca	ctt	tct	cat	tgt	att	gaa	cta	atg	1104
Thr	Thr	Ala	Gly	Ile	Leu	Ala	Thr	Leu	Ser	His	Cys	Ile	Glu	Leu	Met	
				355			360				365					
gtt	aaa	cgt	gag	gac	agc	tgg	cag	aag	aga	ctg	gat	aag	gaa	act	gag	1152
Val	Lys	Arg	Glu	Asp	Ser	Trp	Gln	Lys	Arg	Leu	Asp	Lys	Glu	Thr	Glu	
				370			375				380					
aag	aaa	aga	aga	aca	gag	gaa	gca	tat	aaa	aat	gca	atg	aca	gaa	ctt	1200
Lys	Lys	Arg	Arg	Thr	Glu	Glu	Ala	Tyr	Lys	Asn	Ala	Met	Thr	Glu	Leu	
				385			390				395				400	

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aag	aaa	aaa	tcc	cac	ttt	gga	gga	cca	gat	tat	gaa	gaa	ggc	cct	aac	1248
Lys	Lys	Lys	Ser	His	Phe	Gly	Gly	Pro	Asp	Tyr	Glu	Glu	Gly	Pro	Asn	
405									410					415		
agt	ctg	att	aat	gaa	gaa	gag	ttc	ttt	gat	gct	gtt	gaa	gct	gct	ctt	1296
Ser	Leu	Ile	Asn	Glu	Glu	Glu	Phe	Phe	Asp	Ala	Val	Glu	Ala	Ala	Leu	
420								425					430			
gac	aga	caa	gat	aaa	ata	gaa	gaa	cag	tca	cag	agt	gaa	aag	gtg	aga	1344
Asp	Arg	Gln	Asp	Lys	Ile	Glu	Glu	Gln	Ser	Gln	Ser	Glu	Lys	Val	Arg	
435								440					445			
tta	cat	tgg	cct	aca	tcc	ttg	ccc	tct	gga	gat	gcc	ttt	tct	tct	gtg	1392
Leu	His	Trp	Pro	Thr	Ser	Leu	Pro	Ser	Gly	Asp	Ala	Phe	Ser	Ser	Val	
450								455					460			
ggg	aca	cat	aga	ttt	gtc	caa	aag	gtt	gaa	gag	atg	gtg	cag	aac	cac	1440
Gly	Thr	His	Arg	Phe	Val	Gln	Lys	Val	Glu	Glu	Met	Val	Gln	Asn	His	
465								470					475			480
atg	act	tac	tca	tta	cag	gat	gta	ggc	gga	gat	gcc	aat	tgg	cag	ttg	1488
Met	Thr	Tyr	Ser	Leu	Gln	Asp	Val	Gly	Gly	Asp	Ala	Asn	Trp	Gln	Leu	
485								490					495			
gtt	gta	gaa	gaa	gga	gaa	atg	aag	gta	tac	aga	aga	gaa	gta	gaa	gaa	1536
Val	Val	Glu	Glu	Gly	Glu	Met	Lys	Val	Tyr	Arg	Arg	Glu	Val	Glu	Glu	
500								505					510			
aat	ggg	att	gtt	ctg	gat	cct	tta	aaa	gct	acc	cat	gca	gtt	aaa	ggc	1584
Asn	Gly	Ile	Val	Leu	Asp	Pro	Leu	Lys	Ala	Thr	His	Ala	Val	Lys	Gly	
515								520					525			
gtc	aca	gga	cat	gaa	gtc	tgc	aat	tat	ttc	tgg	aat	gtt	gac	gtt	cgc	1632
Val	Thr	Gly	His	Glu	Val	Cys	Asn	Tyr	Phe	Trp	Asn	Val	Asp	Val	Arg	
530								535					540			
aat	gac	tgg	gaa	aca	act	ata	gaa	aac	ttt	cat	gtg	gtg	gaa	aca	tta	1680
Asn	Asp	Trp	Glu	Thr	Thr	Ile	Glu	Asn	Phe	His	Val	Val	Glu	Thr	Leu	
545								550					555			560
gct	gat	aat	gca	atc	atc	att	tat	caa	aca	cac	aag	agg	gtg	tgg	cct	1728
Ala	Asp	Asn	Ala	Ile	Ile	Ile	Tyr	Gln	Thr	His	Lys	Arg	Val	Trp	Pro	
565								570					575			
gct	tct	cag	cga	gac	gta	tta	tat	ctt	tct	gtc	att	cga	aag	ata	cca	1776
Ala	Ser	Gln	Arg	Asp	Val	Leu	Tyr	Leu	Ser	Val	Ile	Arg	Lys	Ile	Pro	
580								585					590			
gcc	ttg	act	gaa	aat	gac	cct	gaa	act	tgg	ata	gtt	tgt	aat	ttt	tct	1824
Ala	Leu	Thr	Glu	Asn	Asp	Pro	Glu	Thr	Trp	Ile	Val	Cys	Asn	Phe	Ser	
595								600					605			
gtg	gat	cat	gac	agt	gct	cct	cta	aac	aac	cga	tgt	gtc	cgt	gcc	aaa	1872
Val	Asp	His	Asp	Ser	Ala	Pro	Leu	Asn	Asn	Arg	Cys	Val	Arg	Ala	Lys	
610								615					620			
ata	aat	gtt	gct	atg	att	tgt	caa	acc	ttg	gta	agc	cca	cca	gag	gga	1920
Ile	Asn	Val	Ala	Met	Ile	Cys	Gln	Thr	Leu	Val	Ser	Pro	Pro	Glu	Gly	
625								630					635			640
aac	cag	gaa	att	agc	agg	gac	aac	att	cta	tgc	aag	att	aca	tat	gta	1968
Asn	Gln	Glu	Ile	Ser	Arg	Asp	Asn	Ile	Leu	Cys	Lys	Ile	Thr	Tyr	Val	
645								650					655			

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gct aat gtg aac cct gga gga tgg gca cca gcc tca gtg tta agg gca
Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg Ala
660 665 670

2016

gtg gca aag cga gag tat cct aaa ttt cta aaa cgt ttt act tct tac
Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr
675 680 685

2064

gtc caa gaa aaa act gca gga aag cct att ttg ttc tag
Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
690 695 700

2103

<210> 28

<211> 700

<212> PRT

<213> artificial

<220>

<223> Derived sequence

<400> 28

Ala Ser Arg Gly Leu Ser Ser Gly Gly Ser Ala Gly Arg Asn Ala Gly
1 5 10 15

val Thr Ala Thr Ala Ala Ala Asp Gly Trp Lys Gly Arg Leu Pro
20 25 30

Ser Pro Leu Val Leu Leu Pro Arg Ser Ala Arg Cys Gln Ala Arg Arg
35 40 45

Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Leu Pro Pro Thr Pro
50 55 60

Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
65 70 75 80

Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu Leu
85 90 95

Leu Gly Cys Arg Ala Ser Met Ser Asp Asn Gln Ser Trp Asn Ser Ser
100 105 110

Gly Ser Glu Glu Asp Pro Glu Thr Glu Ser Gly Pro Pro Val Glu Arg
115 120 125

Cys Gly Val Leu Ser Lys Trp Thr Asn Tyr Ile His Gly Trp Gln Asp
130 135 140

Arg Trp Val Val Leu Lys Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu
145 150 155 160

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Asp Glu Thr Glu Tyr Gly Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala
165 170 175

Val Ile Thr Pro His Asp Phe Asp Glu Cys Arg Phe Asp Ile Ser Val
180 185 190

Asn Asp Ser Val Trp Tyr Leu Arg Ala Gln Asp Pro Asp His Arg Gln
195 200 205

Gln Trp Ile Asp Ala Ile Glu Gln His Lys Thr Glu Ser Gly Tyr Gly
210 215 220

Ser Glu Ser Ser Leu Arg Arg His Gly Ser Met Val Ser Leu Val Ser
225 230 235 240

Gly Ala Ser Gly Tyr Ser Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly
245 250 255

His Ser Leu Arg Glu Lys Leu Ala Glu Met Glu Thr Phe Arg Asp Ile
260 265 270

Leu Cys Arg Gln Val Asp Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala
275 280 285

Asp Ala Val Ser Lys Asp Glu Leu Gln Arg Asp Lys Val Val Glu Asp
290 295 300

Asp Glu Asp Asp Phe Pro Thr Thr Arg Ser Asp Gly Asp Phe Leu His
305 310 315 320

Ser Thr Asn Gly Asn Lys Glu Lys Leu Phe Pro His Val Thr Pro Lys
325 330 335

Gly Ile Asn Gly Ile Asp Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala
340 345 350

Thr Thr Ala Gly Ile Leu Ala Thr Leu Ser His Cys Ile Glu Leu Met
355 360 365

Val Lys Arg Glu Asp Ser Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu
370 375 380

Lys Lys Arg Arg Thr Glu Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu
385 390 395 400

Lys Lys Lys Ser His Phe Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn
405 410 415

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Ser Leu Ile Asn Glu Glu Glu Phe Phe Asp Ala Val Glu Ala Ala Leu
420 425 430

Asp Arg Gln Asp Lys Ile Glu Glu Gln Ser Gln Ser Glu Lys Val Arg
435 440 445

Leu His Trp Pro Thr Ser Leu Pro Ser Gly Asp Ala Phe Ser Ser Val
450 455 460

Gly Thr His Arg Phe Val Gln Lys Val Glu Glu Met Val Gln Asn His
465 470 475 480

Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala Asn Trp Gln Leu
485 490 495

Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg Glu Val Glu Glu
500 505 510

Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His Ala Val Lys Gly
515 520 525

Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn Val Asp Val Arg
530 535 540

Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val Val Glu Thr Leu
545 550 555 560

Ala Asp Asn Ala Ile Ile Tyr Gln Thr His Lys Arg Val Trp Pro
565 570 575

Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro
580 585 590

Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val Cys Asn Phe Ser
595 600 605

Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys Val Arg Ala Lys
610 615 620

Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro Pro Glu Gly
625 630 635 640

Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val
645 650 655

Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg Ala
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660

665

670

Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr
675 680 685

Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
690 695 700

<210> 29
<211> 13
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 29

Gly Ala Gly Ala Gly Leu Leu Leu Gly Cys Arg Ala Ser
1 5 10

<210> 30
<211> 31
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 30

Pro Ser Pro Asp Pro Ser Pro Arg Gly Leu Gly Ala Ser Ser Gly Ala
1 5 10 15

Ala Glu Gly Ala Gly Ala Gly Leu Leu Leu Gly Cys Arg Ala Ser
20 25 30

<210> 31
<211> 54
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 31

Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Leu Pro Pro Thr Pro
1 5 10 15

Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
20 25 30

Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu Leu
35 40 45

Leu Gly Cys Arg Ala Ser
50

<210> 32
<211> 78
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 32

Asp Gly Trp Lys Gly Arg Leu Pro Ser Pro Leu Val Leu Leu Pro Arg
1 5 10 15

Ser Ala Arg Cys Gln Ala Arg Arg Arg Arg Gly Gly Arg Thr Ser Ser
20 25 30

Leu Leu Leu Leu Pro Pro Thr Pro Glu Arg Ala Leu Phe Ala Ser Pro
35 40 45

Ser Pro Asp Pro Ser Pro Arg Gly Leu Gly Ala Ser Ser Gly Ala Ala
50 55 60

Glu Gly Ala Gly Ala Gly Leu Leu Leu Gly Cys Arg Ala Ser
65 70 75

<210> 33
<211> 102
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 33

Ala Ser Arg Gly Leu Ser Ser Gly Gly Ser Ala Gly Arg Asn Ala Gly
1 5 10 15

Val Thr Ala Thr Ala Ala Ala Asp Gly Trp Lys Gly Arg Leu Pro
20 25 30

Ser Pro Leu Val Leu Leu Pro Arg Ser Ala Arg Cys Gln Ala Arg Arg
35 40 45

Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Leu Pro Pro Thr Pro
50 55 60

Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
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65

70

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75

80

Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu Leu
85 90 95

Leu Gly Cys Arg Ala Ser
100

<210> 34
<211> 103
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 34

Leu Ala Ser Arg Gly Leu Ser Ser Gly Gly Ser Ala Gly Arg Asn Ala
1 5 10 15

Gly Val Thr Ala Thr Ala Ala Ala Asp Gly Trp Lys Gly Arg Leu
20 25 30

Pro Ser Pro Leu Val Leu Leu Pro Arg Ser Ala Arg Cys Gln Ala Arg
35 40 45

Arg Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Leu Pro Pro Thr
50 55 60

Pro Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg
65 70 75 80

Gly Leu Gly Ala Ser Ser Gly Ala Ala Glu Gly Ala Gly Ala Gly Leu
85 90 95

Leu Leu Gly Cys Arg Ala Ser
100

<210> 35
<211> 90
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 35

Leu Ala Ser Arg Gly Leu Ser Ser Gly Gly Ser Ala Gly Arg Asn Ala
1 5 10 15

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Gly Val Thr Ala Thr Ala Ala Ala Ala Asp Gly Trp Lys Gly Arg Leu
20 25 30

Pro Ser Pro Leu Val Leu Leu Pro Arg Ser Ala Arg Cys Gln Ala Arg
35 40 45

Arg Arg Arg Gly Gly Arg Thr Ser Ser Leu Leu Leu Leu Pro Pro Thr
50 55 60

Pro Glu Arg Ala Leu Phe Ala Ser Pro Ser Pro Asp Pro Ser Pro Arg
65 70 75 80

Gly Leu Gly Ala Ser Ser Gly Ala Ala Glu
85 90

<210> 36
<211> 18
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 36

Pro Arg Ser Ala Arg Cys Gln Ala Arg Arg Arg Gly Gly Arg Thr
1 5 10 15

Ser Ser

<210> 37
<211> 897
<212> DNA
<213> artificial

<220>
<223> Derived sequence

<220>
<221> CDS
<222> (1)..(897)
<223>

<400> 37
atg tcg gat aat cag agc tgg aac tcg tcg ggc tcg gag gag gat cca 48
Met Ser Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro
1 5 10 15

gag acg gag tct ggg ccg cct gtg gag cgc tgc ggg gtc ctc agt aag 96
Glu Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys
20 25 30

tgg aca aac tac att cat ggg tgg cag gat cgt tgg gta gtt ttg aaa 144
Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
35 40 45

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aat aat gct ctg agt tac tac aaa tct gaa gat gaa aca gag tat ggc Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly 50 55 60	192
tgc aga gga tcc atc tgt ctt agc aag gct gtc atc aca cct cac gat Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp 65 70 75 80	240
ttt gat gaa tgt cga ttt gat att agt gta aat gat agt gtt tgg tat Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr 85 90 95	288
ctt cgt gct cag gat cca gat cat aga cag caa tgg ata gat gcc att Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile 100 105 110	336
gaa cag cac aag act gaa tct gga tat gga tct gaa tcc agc ttg cgt Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg 115 120 125	384
cga cat ggc tca atg gtg tcc ctg gtg tct gga gca agt ggc tac tct Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser 130 135 140	432
gca aca tcc acc tct tca ttc aag aaa ggc cac agt tta cgt gag aag Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys 145 150 155 160	480
ttg gct gaa atg gaa aca ttt aga gac atc tta tgt aga caa gtt gac Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp 165 170 175	528
acg cta cag aag tac ttt gat gcc tgt gct gat gtc tct aag gat Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp 180 185 190	576
gaa ctt caa agg gat aaa gtg gta gaa gat gat gaa gat gac ttt cct Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro 195 200 205	624
aca acg cgt tct gat ggt gac ttc ttg cat agt acc aac ggc aat aaa Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys 210 215 220	672
gaa aag tta ttt cca cat gtg aca cca aaa gga att aat ggt ata gac Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp 225 230 235 240	720
ttt aaa ggg gaa gcg ata act ttt aaa gca act act gct gga atc ctt Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu 245 250 255	768
gca aca ctt tct cat tgt att gaa cta atg gtt aaa cgt gag gac agc Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser 260 265 270	816
tgg cag aag aga ctg gat aag gaa act gag aag aaa aga aga aca gag Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu 275 280 285	864
gaa gca tat aaa aat gca atg aca gaa ctt aag Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys	897

290

295

<210> 38
 <211> 299
 <212> PRT
 <213> artificial

<220>
 <223> Derived sequence

<400> 38

Met Ser Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro
 1 5 10 15

Glu Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys
 20 25 30

Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
 35 40 45

Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
 50 55 60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
 65 70 75 80

Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
 85 90 95

Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
 100 105 110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
 115 120 125

Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
 130 135 140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
 145 150 155 160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
 165 170 175

Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
 180 185 190

Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
 195 200 205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
210 215 220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225 230 235 240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
245 250 255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
260 265 270

Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
275 280 285

Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys
290 295

<210> 39
<211> 5
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 39

Ser His Cys Ile Glu
1 5

<210> 40
<211> 5
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 40

Ser His Cys Ile Gln
1 5

<210> 41
<211> 10
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 41

Ala Thr Thr Ala Gly Ile Leu Ala Thr Leu
1 5 10

<210> 42
<211> 10
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 42

Leu Met Val Lys Arg Glu Asp Ser Trp Gln
1 5 10

<210> 43
<211> 15
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 43

Ile Leu Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg
1 5 10 15

<210> 44
<211> 15
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 44

Ile Leu Ala Thr Leu Ser His Cys Ile Gln Leu Met Val Lys Arg
1 5 10 15

<210> 45
<211> 10
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 45

Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
1 5 10

<210> 46
<211> 26

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<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 46

Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val Ser Ala
1 5 10 15

Ser Asp Asp Val His Arg Phe Ser Ser Gln
20 25

<210> 47
<211> 21
<212> RNA
<213> artificial

<220>
<223> Derived sequence

<400> 47
aaacuacauu cauggguggc a

21

<210> 48
<211> 21
<212> RNA
<213> artificial

<220>
<223> Derived sequence

<400> 48
aaacagagua uggcugcaga g

21

<210> 49
<211> 21
<212> RNA
<213> artificial

<220>
<223> Derived sequence

<400> 49
aaguacuuug augccugugc u

21

<210> 50
<211> 21
<212> RNA
<213> artificial

<220>
<223> Derived sequence

<400> 50
aaaggcguca caggacauga a

21

<210> 51
 <211> 21
 <212> RNA
 <213> artificial

<220>
 <223> Derived sequence

<400> 51
 aagccuaaua gucgcucuuc c

21

<210> 52
 <211> 244
 <212> PRT
 <213> artificial

<220>
 <223> Derived sequence

<400> 52

Gly Leu Lys Gly Lys Arg Gly Asp Ser Gly Ser Pro Ala Thr Trp Thr
 1 5 10 15

Thr Arg Gly Phe Val Phe Thr Arg His Ser Gln Thr Thr Ala Ile Pro
 20 25 30

Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
 35 40 45

Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
 50 55 60

Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn
 65 70 75 80

Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp
 85 90 95

Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly
 100 105 110

Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro
 115 120 125

Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro Cys
 130 135 140

Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met Phe
 145 150 155 160

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Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro Gly
165 170 175

Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly
180 185 190

Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala
195 200 205

Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val
210 215 220

Lys Ala Gly Glu Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met
225 230 235 240

Lys Lys Arg His

<210> 53
<211> 197
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 53

Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu
1 5 10 15

Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg
20 25 30

His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly
35 40 45

Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Val Pro Trp Leu Lys
50 55 60

Pro Gly Arg Ser Pro Leu Pro Ser His Ala Arg Ser Gln Pro Gly Leu
65 70 75 80

Cys Asn Met Tyr Lys Asp Ser His His Pro Ala Arg Thr Ala His Tyr
85 90 95

Gly Ser Leu Pro Gln Lys Ser His Gly Arg Thr Gln Asp Glu Asn Pro
100 105 110

Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro
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115

120

125

Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser Arg Phe Ser Trp Gly
130 135 140

Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr Gly Gly Arg Ala Ser Asp
145 150 155 160

Tyr Lys Ser Ala His Lys Gly Phe Lys Gly Val Asp Ala Gln Gly Thr
165 170 175

Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg Asp Ser Arg Ser Gly Ser
180 185 190

Pro Met Ala Arg Arg
195

<210> 54

<211> 253

<212> PRT

<213> artificial

<220>

<223> Derived sequence

<400> 54

Met Ala Asn Leu Gly Cys Trp Met Leu Val Leu Phe Val Ala Thr Trp
1 5 10 15

Ser Asp Leu Gly Leu Cys Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn
20 25 30

Thr Gly Gly Ser Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg
35 40 45

Tyr Pro Pro Gln Gly Gly Gly Trp Gly Gln Pro His Gly Gly
50 55 60

Trp Gly Gln Pro His Gly Gly Trp Gly Gln Pro His Gly Gly
65 70 75 80

Trp Gly Gln Pro His Gly Gly Trp Gly Gln Gly Gly Thr His
85 90 95

Ser Gln Trp Asn Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met
100 105 110

Ala Gly Ala Ala Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr
115 120 125

Met Leu Gly Ser Ala Met Ser Arg Pro Ile Ile His Phe Gly Ser Asp
 130 135 140

Tyr Glu Asp Arg Tyr Tyr Arg Glu Asn Met His Arg Tyr Pro Asn Gln
 145 150 155 160

Val Tyr Tyr Arg Pro Met Asp Glu Tyr Ser Asn Gln Asn Asn Phe Val
 165 170 175

His Asp Cys Val Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr
 180 185 190

Thr Lys Gly Glu Asn Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg
 195 200 205

Val Val Glu Gln Met Cys Ile Thr Gln Tyr Glu Arg Glu Ser Gln Ala
 210 215 220

Tyr Tyr Gln Arg Gly Ser Ser Met Val Leu Phe Ser Ser Pro Pro Val
 225 230 235 240

Ile Leu Leu Ile Ser Phe Leu Ile Phe Leu Ile Val Gly
 245 250

<210> 55
 <211> 42
 <212> PRT
 <213> artificial

<220>
 <223> Derived sequence

<400> 55

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
 1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
 20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala
 35 40

<210> 56
 <211> 244
 <212> PRT
 <213> artificial

<220>
 <223> Derived sequence

<400> 56

Gly Leu Lys Gly Lys Arg Gly Asp Ala Gly Ser Pro Ala Thr Trp Thr
 1 5 10 15

Thr Arg Gly Phe Val Phe Thr Arg His Ser Gln Thr Thr Ala Ile Pro
 20 25 30

Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
 35 40 45

Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
 50 55 60

Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn
 65 70 75 80

Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp
 85 90 95

Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly
 100 105 110

Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro
 115 120 125

Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro Cys
 130 135 140

Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met Phe
 145 150 155 160

Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro Gly
 165 170 175

Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly
 180 185 190

Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala
 195 200 205

Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val
 210 215 220

Lys Ala Gly Glu Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met
 225 230 235 240

Lys Lys Arg His

<210> 57
 <211> 244
 <212> PRT
 <213> artificial

<220>
 <223> Derived sequence

<400> 57

Gly Leu Lys Gly Lys Arg Gly Asp Asp Gly Ser Pro Ala Thr Trp Thr
 1 5 10 15

Thr Arg Gly Phe Val Phe Thr Arg His Ser Gln Thr Thr Ala Ile Pro
 20 25 30

Ser Cys Pro Glu Gly Thr Val Pro Leu Tyr Ser Gly Phe Ser Phe Leu
 35 40 45

Phe Val Gln Gly Asn Gln Arg Ala His Gly Gln Asp Leu Gly Thr Leu
 50 55 60

Gly Ser Cys Leu Gln Arg Phe Thr Thr Met Pro Phe Leu Phe Cys Asn
 65 70 75 80

Val Asn Asp Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser Tyr Trp
 85 90 95

Leu Ser Thr Pro Ala Leu Met Pro Met Asn Met Ala Pro Ile Thr Gly
 100 105 110

Arg Ala Leu Glu Pro Tyr Ile Ser Arg Cys Thr Val Cys Glu Gly Pro
 115 120 125

Ala Ile Ala Ile Ala Val His Ser Gln Thr Thr Asp Ile Pro Pro Cys
 130 135 140

Pro His Gly Trp Ile Ser Leu Trp Lys Gly Phe Ser Phe Ile Met Phe
 145 150 155 160

Thr Ser Ala Gly Ser Glu Gly Thr Gly Gln Ala Leu Ala Ser Pro Gly
 165 170 175

Ser Cys Leu Glu Glu Phe Arg Ala Ser Pro Phe Leu Glu Cys His Gly
 180 185 190

Arg Gly Thr Cys Asn Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala
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195 200 205

Ser Leu Asn Pro Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val
210 215 220

Lys Ala Gly Glu Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met
225 230 235 240

Lys Lys Arg His

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<213> artificial

<220>
<223> ON-hmbGPBP

<400> 58
cctccgagcc cgacgagttc

20

<210> 59
<211> 20
<212> DNA
<213> artificial

<220>
<223> ON-dinb1

<400> 59
gaccgaaagg ggcacgcaac

20

<210> 60
<211> 33
<212> DNA
<213> artificial

<220>
<223> ON-GPBP D102

<400> 60
aaaaagaatt cgcatcgagg gggctaagtt cgg

33

<210> 61
<211> 31
<212> DNA
<213> artificial

<220>
<223> ON-GPBP D174

<400> 61
aaaaagaatt cgacggctgg aagggttaggc t

31

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<210> 62
<211> 32
<212> DNA
<213> artificial

<220>
<223> ON-GPBP D246

<400> 62
aaaaagaatt ctgtcaggcg cggcggcggc gc

32

<210> 63
<211> 30
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<213> artificial

<220>
<223> ON-GPBP D315

<400> 63
gacgaattcc catcccccga cccttcaccc

30

<210> 64
<211> 33
<212> DNA
<213> artificial

<220>
<223> ON-GPBP D369

<400> 64
aaaaagaatt cggagcgggg gccggcttcc tgc

33

<210> 65
<211> 20
<212> DNA
<213> artificial

<220>
<223> ON-pU1

<400> 65
acgactcact atagggagac

20

<210> 66
<211> 20
<212> DNA
<213> artificial

<220>
<223> ON-pcDNAC

<400> 66
ctcttagcatt tagtgacac

20

<210> 67
<211> 33
<212> DNA

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<213> artificial

<220>

<223> ON-GPBPMet (mutant)

<400> 67

ggttgcgag cctccggatc ggataatcag agc

33

<210> 68

<211> 30

<212> DNA

<213> artificial

<220>

<223> ON-PrP-F3

<400> 68

gagaattcag cagtcattat ggcgaacctt

30

<210> 69

<211> 31

<212> DNA

<213> artificial

<220>

<223> ON- PrP-R1

<400> 69

gaactcgagc cttcctcatc ccactatcag g

31

<210> 70

<211> 25

<212> DNA

<213> artificial

<220>

<223> ON-E/K-PrP-F6

<400> 70

tatcacccag tacaagaggg aatct

25

<210> 71

<211> 25

<212> DNA

<213> artificial

<220>

<223> ON-E/K-PrP-R6

<400> 71

agattccctc ttgtactggg tgata

25

<210> 72

<211> 22

<212> DNA

<213> artificial

<220>

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<223> ON-E168R-F1

<400> 72

cccatggata ggtacagcaa cc

22

<210> 73

<211> 22

<212> DNA

<213> artificial

<220>

<223> ON-E168R-R1

<400> 73

ggttgctgta cctatccatg gg

22

<210> 74

<211> 25

<212> DNA

<213> artificial

<220>

<223> ON-Q172R-F1

<400> 74

gagtagcagca acaggaacaa ctttg

25

<210> 75

<211> 25

<212> DNA

<213> artificial

<220>

<223> ON-Q172R-R1

<400> 75

caaagggttt cctgttgctg tactc

25

<210> 76

<211> 22

<212> DNA

<213> artificial

<220>

<223> ON-R220A-F1

<400> 76

cagtacgagg cggaaatctca gg

22

<210> 77

<211> 22

<212> DNA

<213> artificial

<220>

<223> ON-R220A-R1

<400> 77

cctgagattc cgcctcgta c tg

<210> 78
 <211> 23
 <212> DNA
 <213> artificial

<220>
 <223> ON-R228A-F1

<400> 78
 tattaccagg caggatcgag cat

<210> 79
 <211> 23
 <212> DNA
 <213> artificial

<220>
 <223> ON-R228A-R1

<400> 79
 atgctcgatc ctgcctggta ata

<210> 80
 <211> 64
 <212> DNA
 <213> artificial

<220>
 <223> SiGPBP/D26-1

<400> 80
 gatcccaacta cattcatggg tggcattcaa gagatgccac ccatgaatgt agtttttttg 60
 gaaa 64

<210> 81
 <211> 64
 <212> DNA
 <213> artificial

<220>
 <223> SiGPBP/D26-1

<400> 81
 agctttcca aaaaaactac attcatgggt ggcattcttt gaatgccacc catgaatgta 60
 gtgg 64

<210> 82
 <211> 64
 <212> DNA
 <213> artificial

<220>
 <223> SiGPBP/D26-2

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<400> 82
gatcccacag agtatggctg cagagttcaa gagactctgc agccatactc tgttttttg 60
gaaa 64

<210> 83
<211> 64
<212> DNA
<213> artificial

<220>
<223> SiGPBP/D26-2

<400> 83
agctttcca aaaaaacaga gtatggctgc agagtctctt gaactctgca gccatactct 60
gtgg 64

<210> 84
<211> 64
<212> DNA
<213> artificial

<220>
<223> SiGPBP/D26-3

<400> 84
gatccgtac tttgatgcct gtgcttcaa gagaagcaca ggcataaag tactttttg 60
gaaa 64

<210> 85
<211> 64
<212> DNA
<213> artificial

<220>
<223> SiGPBP/D26-3

<400> 85
agctttcca aaaaagtact ttgatgcctg tgcttctt gaaagcacag gcatcaaagt 60
acgg 64

<210> 86
<211> 64
<212> DNA
<213> artificial

<220>
<223> SiGPBP/D26-4

<400> 86
gatcccaggc gtcacaggac atgaattcaa gagattcatg tcctgtgacg ccttttttg 60
gaaa 64

<210> 87

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<211> 64
<212> DNA
<213> artificial

<220>
<223> SiGPBP/D26-4

<400> 87
agctttcca aaaaaaggcg tcacaggaca tgaatctctt gaattcatgt cctgtgacgc 60
ctgg 64

<210> 88
<211> 64
<212> DNA
<213> artificial

<220>
<223> SiGPBP

<400> 88
gatcccgccc tatagtcgct cttccttcaa gagaggaaga gcgactatag ggcttttg 60
gaaa 64

<210> 89
<211> 64
<212> DNA
<213> artificial

<220>
<223> SiGPBP

<400> 89
agctttcca aaaaagccct atagtcgctc ttcctcttta gaaggaagag cgactatagg 60
gcgg 64

<210> 90
<211> 14
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 90

Leu Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg
1 5 10

<210> 91
<211> 15
<212> PRT
<213> artificial

<220>
<223> Derived sequence

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<400> 91

Val Leu Met Ala Ser Leu Glu Thr Leu Cys Arg Ile His Lys Ile
1 5 10 15

<210> 92
<211> 22
<212> PRT
<213> artificial

<220>
<223> Derived sequence

<400> 92

Lys Gly Lys Pro Gly Asp Thr Gly Pro Pro Ala Ala Gly Ala Val Met
1 5 10 15

Arg Gly Phe Val Phe Thr
20

<210> 93
<211> 2760
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (138)..(2318)
<223>

<400> 93
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gtgagtgagt ggatctgggt ctctgccgtt ggcttggctc ttcccgctt cctccctcc 120
tccctccctg actgagg ttg gca tct agg ggg ccg agt tca ggt ggc ggc 170
Leu Ala Ser Arg Gly Pro Ser Ser Gly Gly Gly
1 5 10
gcc ggg cgc agc gca ggg gtc acg gcc acg gcg gct gac ggc tgg aag 218
Ala Gly Arg Ser Ala Gly Val Thr Ala Thr Ala Ala Asp Gly Trp Lys
15 20 25
ggc agg ctt tct tcg ccg ctc gtc ctc ctt ccc cgg tcc gct cgg tgt 266
Gly Arg Leu Ser Ser Pro Leu Val Leu Leu Pro Arg Ser Ala Arg Cys
30 35 40
cag gcg cgg cgg cgg cgc ggc ggg cgc gct tcg tcc ctc ttc ctg 314
Gln Ala Arg Arg Arg Arg Arg Gly Gly Arg Ala Ser Ser Leu Phe Leu
45 50 55
ttc cct cac tcc ccg gag cgg gct ctc ttg gcg gtg cca tcc ccc gac 362
Phe Pro His Ser Pro Glu Arg Ala Leu Leu Ala Val Pro Ser Pro Asp
60 65 70 75
cct tca ccc cag gga cta ggc gcc tgc act ggc gca gct cgc gga gcg 410
Pro Ser Pro Gin Gly Leu Gly Ala Cys Thr Gly Ala Ala Arg Gly Ala
80 85 90

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Gly	Ala	Gly	Leu	Leu	Leu	Gly	Cys	Arg	Val	Ser	Met	Ser	Asp	Asn	Gln	
95								100					105			
agc	tgg	aac	tcg	tcg	ggc	tcg	gag	gag	gat	ccg	gag	acg	gag	tcc	ggg	506
Ser	Trp	Asn	Ser	Ser	Gly	Ser	Glu	Glu	Asp	Pro	Glu	Thr	Glu	Ser	Gly	
110							115				120					
ccg	cct	gtg	gag	cgc	tgc	ggg	gtc	ctc	agc	aag	tgg	aca	aac	tat	att	554
Pro	Pro	Val	Glu	Arg	Cys	Gly	Val	Leu	Ser	Lys	Trp	Thr	Asn	Tyr	Ile	
125							130				135					
cat	gga	tgg	cag	gat	cgt	tgg	gta	gtt	ttg	aaa	aat	aat	act	ttg	agt	602
His	Gly	Trp	Gln	Asp	Arg	Trp	Val	Val	Leu	Lys	Asn	Asn	Thr	Leu	Ser	
140							145			150				155		
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Tyr	Tyr	Lys	Ser	Glu	Asp	Glu	Thr	Glu	Tyr	Gly	Cys	Arg	Gly	Ser	Ile	
160									165					170		
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Cys	Leu	Ser	Lys	Ala	Val	Ile	Thr	Pro	His	Asp	Phe	Asp	Glu	Cys	Arg	
175								180						185		
ttt	gat	atc	agt	gta	aat	gat	agt	gtt	tgg	tac	ctt	cga	gct	cag	gac	746
Phe	Asp	Ile	Ser	Val	Asn	Asp	Ser	Val	Trp	Tyr	Leu	Arg	Ala	Gln	Asp	
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Pro	Glu	His	Arg	Gln	Gln	Trp	Val	Asp	Ala	Ile	Glu	Gln	His	Lys	Thr	
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gaa	tcg	gga	tat	gga	tct	gag	tcc	agc	ttg	cgt	aga	cat	ggc	tca	atg	842
Glu	Ser	Gly	Tyr	Gly	Ser	Glu	Ser	Ser	Leu	Arg	Arg	Arg	His	Gly	Ser	Met
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Val	Ser	Leu	Val	Ser	Gly	Ala	Ser	Gly	Tyr	Ser	Ala	Thr	Ser	Thr	Ser	
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Ser	Phe	Lys	Lys	Gly	His	Ser	Leu	Arg	Glu	Lys	Leu	Ala	Glu	Met	Glu	
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Thr	Phe	Arg	Asp	Ile	Leu	Cys	Arg	Gln	Val	Asp	Thr	Leu	Gln	Lys	Tyr	
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Phe	Asp	Val	Cys	Ala	Asp	Ala	Val	Ser	Lys	Asp	Glu	Leu	Gln	Arg	Asp	
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gga	gac	ttt	ttg	cac	aat	acc	aat	ggt	aat	aaa	gaa	aaa	tta	ttt	cca	1130
Gly	Asp	Phe	Leu	His	Asn	Thr	Asn	Gly	Asn	Lys	Glu	Lys	Leu	Phe	Pro	
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cat	gta	aca	cca	aaa	gga	att	aat	ggc	ata	gac	ttt	aaa	ggg	gaa	gca	1178
His	Val	Thr	Pro	Lys	Gly	Ile	Asn	Gly	Ile	Asp	Phe	Lys	Gly	Glu	Ala	
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380	385	390
gtg atg gaa gaa ctt aag aag aaa ccc cgt ttc gga ggg ccg gat tat	Val Met Glu Glu Leu Lys Lys Pro Arg Phe Gly Gly Pro Asp Tyr	1370
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445	450	455
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525	530	535
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25

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Val Ile Thr Pro His Asp Phe Asp Glu Cys Arg Phe Asp Ile Ser Val
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His Ser Leu Arg Glu Lys Leu Ala Glu Met Glu Thr Phe Arg Asp Ile
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Asn Thr Asn Gly Asn Lys Glu Lys Leu Phe Pro His Val Thr Pro Lys
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Gly Ile Asn Gly Ile Asp Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala
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Thr Thr Ala Gly Ile Leu Ala Thr Leu Ser His Cys Ile Glu Leu Met
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Lys Arg Arg Arg Val Glu Glu Ala Tyr Lys Asn Val Met Glu Glu Leu
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Lys Lys Lys Pro Arg Phe Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn
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Ser Leu Ile Asn Glu Glu Glu Phe Phe Asp Ala Val Glu Ala Ala Leu
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Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu
515 520 525

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Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile
580 585 590

Val Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val
595 600 605

Leu Tyr Leu Ser Ala Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp
610 615 620

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
625 630 635 640

Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Ile Ala Met Ile
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Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asp Gln Glu Ile Ser Arg
660 665 670

Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly
675 680 685

Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
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Gly Lys Pro Ile Leu Phe
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 tccctccctg actgagg ttg gca tct agg ggg ccg agt tca ggt ggc ggc 170
 Leu Ala Ser Arg Gly Pro Ser Ser Gly Gly Gly
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 gcc ggg cgc agc gca ggg gtc acg gcc acg gcg gct gac ggc tgg aag 218
 Ala Gly Arg Ser Ala Gly Val Thr Ala Thr Ala Ala Asp Gly Trp Lys
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 ggc agg ctt tct tcg ccg ctc gtc ctc ctt ccc cgg tcc gct cgg tgt 266
 Gly Arg Leu Ser Ser Pro Leu Val Leu Leu Pro Arg Ser Ala Arg Cys
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 Gln Ala Arg Arg Arg Arg Gly Gly Arg Ala Ser Ser Leu Phe Leu
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 Phe Pro His Ser Pro Glu Arg Ala Leu Leu Ala Val Pro Ser Pro Asp
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 Pro Ser Pro Gln Gly Leu Gly Ala Cys Thr Gly Ala Ala Arg Gly Ala
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 Gly Ala Gly Leu Leu Leu Gly Cys Arg Val Ser Met Ser Asp Asn Gln
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 Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr Asn Tyr Ile
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 Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp Glu Cys Arg
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 Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg Ala Gln Asp
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 ccg gag cac aga cag caa tgg gta gac gcc att gaa cag cac aag act 794
 Pro Glu His Arg Gln Gln Trp Val Asp Ala Ile Glu Gln His Lys Thr
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Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu Ala Glu Met Glu				
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Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr Leu Gln Lys Tyr				
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Cys Ile Glu Leu Met Val Lys Arg Glu Glu Ser Trp Gln Lys Arg His				
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445	450	455		
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 145 150 155 160

Asp Glu Thr Glu Tyr Gly Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala
 165 170 175

Val Ile Thr Pro His Asp Phe Asp Glu Cys Arg Phe Asp Ile Ser Val
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180

185

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Gln Trp Val Asp Ala Ile Glu Gln His Lys Thr Glu Ser Gly Tyr Gly
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Glu Arg Ala Leu Leu Pro Ser Pro Ser Pro Asp Pro Ser Pro Arg Gly
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Leu Gly Ala Ser Thr Gly Ala Ala Gln Gly Ala Gly Ala Gly Leu Leu
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Cys	Asn	Tyr	Phe	Trp	Asn	Val	Asp	Val	Arg	Asn	Asp	Trp	Glu	Thr	Thr	
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Leu	Tyr	Leu	Ser	Ala	Ile	Arg	Lys	Ile	Pro	Ala	Leu	Asn	Glu	Asn	Asp	
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Lys Arg Arg Arg Val Glu Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu	
390 395 400	
aag aaa aaa tcc cac ttt gga gga cca gat tat gag gaa ggc cca aac	1362
Lys Lys Lys Ser His Phe Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn	
405 410 415 420	
agt ttg att aat gaa gag gag ttc ttt gat gct gtt gaa gct gct ctt	1410
Ser Leu Ile Asn Glu Glu Phe Phe Asp Ala Val Glu Ala Ala Leu	
425 430 435	
gac aga caa gat aaa ata gaa gaa cag tcg cag agt gaa aag gtc agg	1458
Asp Arg Gln Asp Lys Ile Glu Glu Gln Ser Gln Ser Glu Lys Val Arg	
440 445 450	
tta cat tgg tct act tca atg cca tct gga gat gcc ttt tct tct gtg	1506
Leu His Trp Ser Thr Ser Met Pro Ser Gly Asp Ala Phe Ser Ser Val	
455 460 465	
ggg act cat aga ttt gtc caa aag gtt gaa gag atg gtg cag aac cac	1554
Gly Thr His Arg Phe Val Gln Lys Val Glu Glu Met Val Gln Asn His	
470 475 480	
atg acc tat tca ttg cag gat gta ggt ggg gac gcc aac tgg cag ttg	1602
Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala Asn Trp Gln Leu	
485 490 495 500	
gtt gta gaa gaa ggg gag atg aag gta tat aga aga gaa gta gaa gaa	1650
Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg Glu Val Glu Glu	
505 510 515	
aat ggg att gtt ctg gat cct ttg aaa gct acc cat gca gtt aaa ggc	1698
Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His Ala Val Lys Gly	
520 525 530	
gtt aca gga cac gag gtc tgc aat tac ttc tgg aat gtt gat gtt cgc	1746
Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn Val Asp Val Arg	
535 540 545	
aat gat tgg gaa aca act ata gaa aac ttt cat gtg gtg gaa aca tta	1794
Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val Val Glu Thr Leu	
550 555 560	
gct gat aat gca atc atc att tat caa acg cac aag aga gtg tgg cca	1842
Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys Arg Val Trp Pro	
565 570 575 580	
gcc tct cag cgg gat gtc tta tat ctg tct gcc att cga aag ata cca	1890
Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Ala Ile Arg Lys Ile Pro	
585 590 595	
gct ttg aat gaa aat gac ccg gag act tgg ata gtt tgt aat ttt tct	1938
Ala Leu Asn Glu Asn Asp Pro Glu Thr Trp Ile Val Cys Asn Phe Ser	

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600	605	610	
gta gat cac agc agt gct cct cta aac aat cga tgt gtc cgt gcc aaa Val Asp His Ser Ser Ala Pro Leu Asn Asn Arg Cys Val Arg Ala Lys 615 620 625			1986
ata aac gtt gct atg att tgt cag acc ttg gtg agc ccc cca gag gga Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro Pro Glu Gly 630 635 640			2034
aac cag gag att agc agg gac aac att cta tgc aag att aca tac gtg Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val 645 650 655 660			2082
gcc aat gta aac cct gga gga tgg gcc cca gcc tca gtg tta cgg gca Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg Ala 665 670 675			2130
gtg gca aag cga gaa tat cca aag ttt cta aag cgt ttt act tct tac Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr 680 685 690			2178
gta caa gaa aaa act gca gga aaa cct att ttg ttc tag tattaacagt Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe 695 700			2227
gactgaagca aggctgtgt acattccatg ttggaggaaa aaaaaaaaaaaa aaaaaa 2283			

<210> 100
 <211> 704
 <212> PRT
 <213> Bos taurus

<400> 100

Leu Ala Ser Arg Gly Pro Asn Ser Gly Gly Gly Ala Gly Arg Ser Ala
1 5 10 15

Gly Val Thr Thr Ala Thr Ala Asp Gly Trp Lys Gly Arg Leu Pro
20 25 30

Ser Pro Leu Asp Leu Leu Pro Arg Ser Ala Trp Cys Gln Ala Arg Arg
35 40 45

Arg Arg Arg Arg Arg Gly Gly Arg Thr Pro Ser Leu Leu Pro Leu
50 55 60

Pro Pro Ala Pro Glu Arg Ala Leu Leu Pro Ser Pro Ser Pro Asp Pro
65 70 75 80

Ser Pro Arg Gly Leu Gly Ala Ser Thr Gly Ala Ala Gln Gly Ala Gly
85 90 95

Ala Gly Leu Leu Leu Gly Cys Arg Ala Ser Met Ser Asp Asn Gln Ser
100 105 110

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Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro Glu Thr Glu Ser Gly Pro
115 120 125

Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr Asn Tyr Ile His
130 135 140

Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn Thr Leu Ser Tyr
145 150 155 160

Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly Cys Arg Gly Ser Ile Cys
165 170 175

Leu Ser Lys Ala Val Ile Thr Pro His Asp Phe Asp Glu Cys Arg Phe
180 185 190

Asp Ile Ser Val Asn Asp Ser Val Trp Tyr Leu Arg Ala Gln Asp Pro
195 200 205

Asp His Arg Gln Gln Trp Ile Asp Ala Ile Glu Gln His Lys Thr Glu
210 215 220

Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg Arg His Gly Ser Met Val
225 230 235 240

Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser Ala Thr Ser Thr Ser Ser
245 250 255

Phe Lys Lys Gly His Ser Leu Arg Glu Lys Leu Ala Glu Met Glu Thr
260 265 270

Phe Arg Asp Ile Leu Cys Arg Gln Val Asp Thr Leu Gln Lys Phe Phe
275 280 285

Asp Ala Cys Ala Asp Ala Val Ser Lys Asp Glu Phe Gln Arg Asp Lys
290 295 300

Val Val Glu Asp Asp Glu Asp Asp Phe Pro Thr Thr Arg Ser Asp Gly
305 310 315 320

Asp Phe Leu His Asn Thr Asn Gly Asn Lys Glu Lys Val Phe Pro His
325 330 335

Val Thr Pro Lys Gly Ile Asn Gly Ile Asp Phe Lys Gly Glu Ala Ile
340 345 350

Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu Ala Thr Leu Ser His Cys
355 360 365

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Ile Glu Leu Met Val Lys Arg Glu Asp Ser Trp Gln Lys Arg Met Asp
370 375 380

Lys Glu Thr Glu Lys Arg Arg Arg Val Glu Glu Ala Tyr Lys Asn Ala
385 390 395 400

Met Thr Glu Leu Lys Lys Ser His Phe Gly Gly Pro Asp Tyr Glu
405 410 415

Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu Glu Phe Phe Asp Ala Val
420 425 430

Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu Glu Gln Ser Gln Ser
435 440 445

Glu Lys Val Arg Leu His Trp Ser Thr Ser Met Pro Ser Gly Asp Ala
450 455 460

Phe Ser Ser Val Gly Thr His Arg Phe Val Gln Lys Val Glu Glu Met
465 470 475 480

Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
485 490 495

Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
500 505 510

Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
515 520 525

Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
530 535 540

Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
545 550 555 560

Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys
565 570 575

Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Ala Ile
580 585 590

Arg Lys Ile Pro Ala Leu Asn Glu Asn Asp Pro Glu Thr Trp Ile Val
595 600 605

Cys Asn Phe Ser Val Asp His Ser Ser Ala Pro Leu Asn Asn Arg Cys
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610

615

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620

Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
625 630 635 640

Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
645 650 655

Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
660 665 670

Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
675 680 685

Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
690 695 700

<210> 101

<211> 13

<212> PRT

<213> Mus musculus

<400> 101

Gly Ala Gly Ala Gly Leu Leu Leu Gly Arg Cys Val Ser
1 5 10

<210> 102

<211> 171

<212> PRT

<213> artificial

<220>

<223> Derived sequence

<400> 102

Met Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu
1 5 10 15

Ala Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg
20 25 30

His Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly
35 40 45

Asp Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro
50 55 60

Ala Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg
65 70 75 80

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Thr Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr
85 90 95

Pro Arg Thr Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu
100 105 110

Ser Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr
115 120 125

Gly Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly
130 135 140

Val Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg
145 150 155 160

Asp Ser Arg Ser Gly Ser Pro Met Ala Arg Arg
165 170

<210> 103

<211> 18

<212> PRT

<213> artificial

<220>

<223> Derived sequence

<400> 103

Pro Arg Ser Ala Arg Cys Gln Ala Arg Arg Arg Arg Gly Gly Arg Thr
1 5 10 15

Ser Ser